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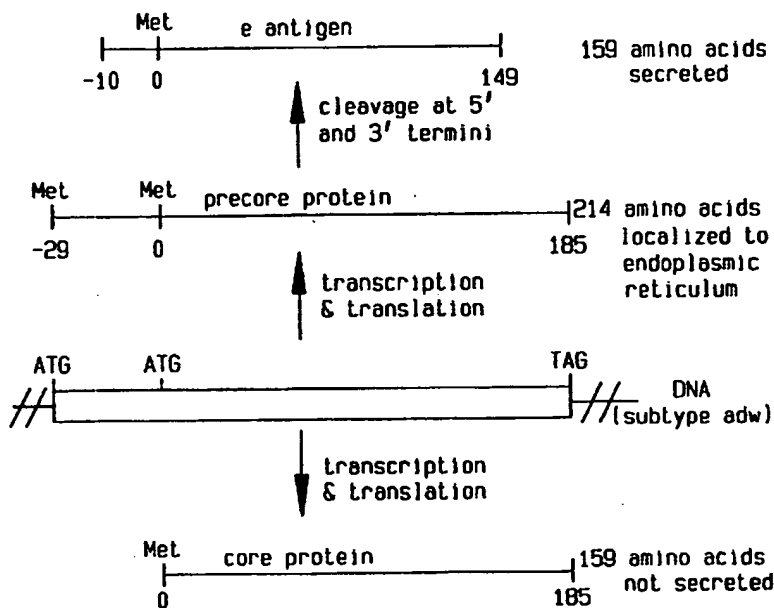
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(54) Title: HEPATITIS B VIRUS VACCINES

(57) Abstract

The present invention provides recombinant vaccinia viruses which are capable of expressing a plurality of immunogenic HBV epitopes comprising at least one core antigen epitope, at least one surface antigen epitope, or any combination of the foregoing. Preferred viruses containing plural HBV antigens include but are not limited to a combination of one of S, MS, LS, and full-length core, core-Δ8 (a core deletion mutant), preS1-core-Δ8, preS1-complete core, core-preS1*, core-preS2, or core-S* (the asterisks denoting the presence of an immunogenic fragment of the preceding antigen; hyphens denoting a fusion protein). As shown in the figure, the core and/or surface antigen epitopes can be expressed by the same recombinant virus, under the control of different promoters active in vaccinia virus.

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HEPATITIS B VIRUS VACCINES

1. INTRODUCTION

The present invention relates to recombinant
5 vaccinia viruses which are capable of expressing a
plurality of hepatitis B virus (HBV) epitopes
comprising core antigen epitopes, surface antigen
epitopes, or any combination of the foregoing. The
vaccinia viruses are useful in vaccine formulations to
10 prevent or treat hepatitis or other undesirable
consequences of HBV infection.

2. BACKGROUND OF THE INVENTION

15 2.1. HEPATITIS B VIRUS

Hepadnaviruses, which include human
hepatitis B virus (HBV) (Barker et al., 1975, Am. J.
Med. Sci. 270:189-196), are hepatropic, lead to
persistent infection, and have a common structure.
20 Large concentrations of hepadnaviruses have been
detected in the blood of infected organisms.
Hepadnavirus virions are approximately 42 nm in
diameter and have a double-walled structure consisting
of an envelope and nucleocapsid (reviewed in Ganem and
25 Varmus, 1987, Ann. Rev. Biochem. 56:651-693 and
Tiollais et al., 1985, Nature (London) 317:489-495).
The outer coat, or envelope, contains three surface
antigens, designated major or small (S), middle (MS),
and large (LS), as well as carbohydrates and lipids.
30 Hepatitis B surface antigen (HBsag) is found on all
three of these surface antigen proteins. The
nucleocapsid, or inner coat, contains a circular DNA
(3.0-3.3 kb in length), a DNA polymerase, protein
kinase activity, and hepatitis B core antigen (HBcAg).
35

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The hepadnavirus genome is a small, circular, partly double stranded DNA molecule (reviewed in Ganem and Varmus, *supra*, and Tiollais et al., *supra*). The minus strand is linear and of a
5 fixed length, 3-3.2 kb. In contrast, the plus strand is of variable length, ranging from 50-100% of that of the minus strand.

The results from analyses of nucleotide sequences of the cloned HBV genome indicated that the
10 minus strand contains four major open reading frames (ORFs), S, C, P, and X (reviewed in Ganem and Varmus, *supra*, and Tiollais, *supra*). ORF S encodes a total of 389-400 amino acids, depending upon subtype. ORF S is divided into the preS1 region (encoding 108-119 amino
15 acids), preS2 region (encoding 55 amino acids), and S gene (encoding 226 amino acids) in 5' to 3' order, each of which begins with an ATG codon capable of functioning as a translation initiation site *in vivo*. Gene S encodes small (S) antigen, the HBsAg, which is
20 the major envelope protein. A 500 nucleotide sequence upstream of the S gene contains the preS1 and preS2 sequences. Middle (MS) protein is encoded by the preS2 and S regions, and large (LS) protein is encoded by the preS1, preS2 and S regions. ORF C, which codes
25 for HBcAg, is divided into the C gene and pre-C region. ORF P encodes the viral polymerase. ORF X encodes a protein which enhances expression of the other viral genes.

Core-related antigen production *in vivo* is a
30 complex process involving two different precursors, precore and core, and post translational truncation at both amino and carboxy termini (Fig. 1). Two main forms of core-related antigens result from this processing: e antigen, which is made from precore and
35 found mainly extracellularly in infected individuals,

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and core, which is found almost exclusively intracellularly, usually within the nucleus of the cell. Putative nuclear localization sequences of the hepatitis B core protein include a set of direct
5 repeats having the amino acid sequence PRRRRSQS (SEQ ID NO:1) located in tandem in the protamine-like domain of core. Yeh et al. (1990, J. Virol. 64:6141-6147) suggest that these repeats are necessary for nuclear localization. Eckhardt et al. (1991, J.
10 Virol. 65:575-582) suggest that other sequences may also be involved.

The structure and expression of the hepatitis B viral genome has been studied by recombinant DNA techniques. U.K. Patent Publication
15 No. GB 2034323A (published June 4, 1980) discloses the cloning and expression of HBV DNA. Moriarty et al. (1981, Proc. Natl. Acad. Sci. USA 78:2606-2610) describes the construction and expression of a recombinant simian virus containing a fragment of HBV
20 DNA encoding the HBsAg; 22 nm surface antigen particles were shown to be excreted into the cell culture medium. European Patent Publication No. 0020251 (published December 10, 1980) describes the construction of and expression from recombinant
25 expression vectors encoding HBV proteins. European Patent Publication No. 0013828 (published August 6, 1980) discloses recombinant DNA vectors which contain fragments of HBV DNA, isolated from Dane particles, which encode proteins with HBV antigenicity.

30

2.2. BIOLOGY OF HBV INFECTION

The liver disease called hepatitis B is a widespread and serious health problem resulting from infection by the hepatitis B virus. A large
35 proportion of people living in regions of poor medical

care are chronically infected with the virus and also face an elevated risk of acquiring liver cancer, since HBV is associated with liver carcinoma. HBV is endemic in Asia, and causes one of the largest health problems in that region, where about 10% of the population are chronically infected carriers. The toll of this figure on the health of Asians is severe; in addition to the impact of acute HBV infection, chronic carriers are at vastly increased risk from cirrhosis and primary hepatocellular carcinoma (PHC). PHC is the second most prevalent cancer in Asia, accounting for up to 22% of cancer deaths in some countries.

HBV infection has been observed to be highly polymorphic, ranging from inapparent forms in which individuals experience mild or no liver injury to acute hepatitis B, a moderately severe illness characterized by hepatocellular injury and inflammation to severe chronic liver disease (reviewed in Ganem and Varmus, 1987, Ann. Rev. Biochem. 56:651-693). People infected with HBV are often unaware of it. After a two- to six-month incubation period, HBV infection can lead to acute hepatitis and liver damage, which cause abdominal pain, jaundice, elevated levels of certain enzymes in the blood and other symptoms. At this stage, hepatitis B viral infection can be diagnosed by detecting hepatitis B surface antigen (HBsAg) in a patient's blood serum. More frequently, the disease remains permanently asymptomatic. Although many chronic carriers appear healthy, they can still transmit the hepatitis B virus to those with whom they have close contact, thereby starting the cycle of disease anew.

Variation in host immune response to virus infected cells appears to be a major determinant in

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the degree of severity of liver damage in individuals. Both humoral and cellular immune responses to HBcAg and HBsAg have generally been observed during acute and chronic HBV infection (reviewed in Robinson, 1986, 5 *Fundamental Virology*, Fields, B.N. and Knipe, D.M. (eds.), Raven Press, N.Y., pp. 657-679).

In addition to causing acute and chronic liver disease, results from epidemiological and molecular biological studies indicate a connection 10 between hepadnavirus infection and hepatoma (liver cancer) (reviewed in Ganem and Varmus, *supra*; Machowiak, 1987, *Am. J. Med.* 82:79-97; and Tiollais et al., 1985, *Nature (London)* 317:489-495. There is a strong correlation between high rates of chronic HBV 15 infection and incidence of hepatoma, e.g., in Southeast Asia and equatorial Africa.

Usually a patient with acute hepatitis will recover completely from the disease. After recovery, the patient continues to produce low levels of 20 antibodies specific for HBV, and thus is immune to HBV for several years. In the event of a new HBV attack, the antibody level rises quickly and neutralizes the virus. In chronically-infected patients, the virus survives in the liver, and may cause cirrhosis and, 25 eventually, hepatocarcinoma. Chronic infection occurs in approximately 5-10% of infected adults and 80% of infected infants. Hepatitis B is, therefore, primarily a disease of infants in developing countries, and is mostly confined to adults in Western 30 countries.

2.3. VACCINATION AND THERAPIES FOR HBV INFECTION

Current methods used to treat HBV infection 35 may be divided into two categories, antivirals and immunomodulatory agents (reviewed in Hoofnagle, Ann.

Int. Med. 107:414-415). One analog that has been widely tested is vidarabine (adenine arabinoside), an adenine analog with potent activity against herpesviruses. While the inhibition of viral replication was observed to be nearly complete and sustained in some patients, the inhibition of replication was partial and transient in other patients. One drawback involved in using this drug is that it is highly water insoluble and has to be administered intravenously as a constant infusion. A monophosphorylated derivative of vidarabine, vidarabine phosphate, can be administered by rapid intravenous infusion or intramuscularly. Even though vidarabine phosphate therapy resulted in the clearance of serum hepatitis B virus DNA, it did not lead to a sustained improvement in the accompanying liver disease. Other antivirals that have been tested for their effectiveness in treating HBV infection include acyclovir and suramin.

Studies have also been undertaken in which patients were treated with alpha-interferons for 1-6 months. It was found that only 25-40% of the patients responded to this therapy. The combination of vidarabine phosphate and human leukocyte interferon proved to be toxic. Other therapies that have been studied include the administration of interleukin-2, gamma interferon, and short course corticosteroids.

U.S. Patent No. 4,471,901 discloses a vaccine comprising a 22 nm polypeptide particle made of mature hepatitis B surface antigen.

Szmuness et al. (1981, J. Med. Virol. 8:123) report that 2-4% of the general population are nonresponsive to the existing recombinant hepatitis vaccine, which contains only the S antigen. Milich et al. (1986, J. Immunol. 137:315) suggest that this lack

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of an anti-S response may be overcome by immunizing with preS epitopes in combination with S. Neurath et al. (EPO publication no. 243,913) disclose an HBV vaccine which includes amino acid sequences from within the preS region of the HBV surface antigen linked to a lipid vesicle. Other groups disclose various surface antigen constructs for vaccine use (U.S. Patent No. 4,816,564; U.S. Patent No. 4,683,136; PCT International Publication No. WO 8810301).

10 Immunization of chimpanzees with recombinant or purified HBcAg has been shown to have some protective effect against HBV challenge (Tabor and Geretz, 1984, Lancet i:172; Murray et al., 1984, EMBO J. 3:645). However, vaccines employing purified HBV antigens are

15 disadvantageous due to the laborious purification procedures required.

A number of groups have made constructs consisting of fusions to the core antigen expressed in bacteria, yeast or vaccinia (see, e.g., U.S. Patent

20 No. 4,859,465; U.S. Patent Nos. 4,818,527 and 4,882,145). In some cases core particles are formed which expose the foreign antigenic determinants on their surface (Clarke et al., 1987, Nature 330:381-384; Borisova et al., FEBS Letters

25 259:121-124).

Potential live vaccines consisting of vaccinia virus recombinants expressing HBV surface antigens have been reported (Smith et al., 1983, Nature 302:490-495; Cheng and Moss, 1987, J. Virol.

30 61(4):1286-1290; Cheng et al., 1986, J. Virol. 60(2):337-344; Paoletti et al., 1984, Proc. Natl. Acad. Sci. USA 81:193-197; Moss et al., 1984, Nature 311:67-69; U.S. patent application Serial No. 6-445,892 filed December 1, 1982).

2.4. VACCINIA VIRUS

Vaccinia virus is a poxvirus (for a review, see Moss, 1990, *Virology*, 2d ed., Ch. 74, Fields et al., eds., Raven Press, Ltd., New York, pp. 2079-2111) which replicates within the cytoplasm of infected cells. Vaccinia virus contains a linear double-stranded genome of approximately 187 kilobase pairs, encoding approximately 200 proteins. A large number of proteins are encoded by the virus because the virus establishes infection in the cytoplasm of the cell rather than in the nucleus, and therefore must provide its own set of enzymes to replicate its DNA and to transcribe its genes.

A vaccine approach has been described, involving the use of vaccinia virus as a vector to express foreign genes inserted into its genome (Mackett et al., 1982, *Proc. Natl. Acad. Sci. USA* 79:7415-7419; Mackett et al., 1984, *J. Virol.* 49:857-864; Panicali and Paoletti, 1982, *Proc. Natl. Acad. Sci. USA* 79:4927-4931; PCT International Application No. W0 91/12318; European Patent Publication No. 83,286; Murphy, 1989, *Res. Virol.* 140:463-491; Moss and Flexner, 1987, *Ann. Rev. Immunol.* 5:305-324; Hruby, 1990, *Clin. Microbiol. Rev.* 3(2):153-170; U.S. Patent No. 4,603,112; U.S. Patent No. 4,722,848; U.S. patent application Serial No. 7-072,455 filed July 13, 1987). Upon introduction into host animals, the recombinant vaccinia virus expresses the inserted foreign gene and may thereby elicit a host immune response to such gene products.

3. SUMMARY OF THE INVENTION

The present invention provides recombinant vaccinia viruses which are capable of expressing a plurality of immunogenic HBV epitopes comprising at

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least one core antigen epitope, at least one surface antigen epitope, or any combination of the foregoing. In one embodiment, a plurality of core and/or surface antigen epitopes is expressed. Core antigen epitopes
5 are selected from the group consisting of wild-type core antigen, e antigen, and derivatives thereof. Surface antigen epitopes are those encoded by ORF S, and are selected from the group consisting of S, MS, LS, preS2, preS1, and derivatives thereof. "Epitope"
10 as used herein refers to an antigenic determinant, i.e., an amino acid sequence that is capable of being immunospecifically bound by an antibody. Thus, for example, a protein containing a core antigen epitope can be detected by observing the ability of such
15 protein to be bound by an anti-core protein antibody. The core antigen derivatives provided by the invention are those derivatives (including but not limited to fragments) which display core antigen antigenicity, i.e., are capable of being bound by an anti-core
20 antibody. Similarly, the surface antigen derivatives provided by the invention are those derivatives (including but not limited to fragments) which display surface antigen antigenicity, i.e., are capable of being bound by an anti-surface antigen antibody.
25 In a specific embodiment, a combination of the foregoing core and/or surface antigen epitopes are expressed as a fusion protein in the vaccinia viruses of the invention. "Fusion protein," as used herein, refers to a protein comprising an amino acid sequence
30 from a first protein covalently linked via a peptide bond at its carboxy terminus to the amino terminus of an amino acid sequence from a second, different protein.

In one embodiment, a vaccine formulation of
35 the invention contains a single type of recombinant

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vaccinia virus of the invention. In another embodiment, a vaccine formulation comprises a mixture of two or more recombinant viruses of the invention. Preferred viruses containing plural HBV antigens
5 include but are not limited to a combination of one of S, MS, LS, and full-length core, core Δ 8 (see Section 6.1.2 *infra*), preS1-core Δ 8, preS1-complete core, core-preS1*, core-preS2, or core-S* (the asterisks denoting the presence of an immunogenic fragment of
10 the preceding antigen; hyphens denoting a fusion protein).

In various embodiments, the core and/or surface antigen epitopes can be expressed by the same recombinant virus, under the control of different
15 promoters active in vaccinia virus. In a preferred aspect, two divergently oriented promoters are used. In a specific embodiment, a recombinant vaccinia virus expresses a surface-core (written in the amino to carboxy-terminal order) or core-surface fusion protein
20 (e.g., core-preS1, core-preS2, core-S, or preS1-core) under the control of a first promoter, and expresses a surface antigen (e.g., MS) under the control of a second promoter.

In another specific embodiment, a mixture of
25 recombinant vaccinia viruses is provided. In one embodiment, such a mixture comprises a first virus capable of expressing core-preS1, a second virus capable of expressing core-preS2, and a third virus capable of expressing core-S or core-S*. In another
30 embodiment, such a mixture comprises a first virus capable of expressing core-preS1 or core-preS1*, a second virus capable of expressing core-preS2, and a third virus capable of expressing S. In another embodiment, such a mixture comprises a first virus
35 capable of expressing core-preS1 or core-preS1*, and a

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second virus capable of expressing MS. In yet another embodiment, such a mixture comprises a first virus capable of expressing core-preS2, and a second virus capable of expressing S.

5

4. DESCRIPTION OF THE FIGURES

Figure 1. Schematic diagram of HBV precore and core processing to produce core antigen and e antigen.

10 Figure 2. Nucleotide sequence (SEQ ID NO:2) of the p7.5 promoter.

Figure 3. Schematic diagram of plasmid pGS53.

15 Figure 4. Nucleotide sequence (SEQ ID NO:3) of the p11 promoter.

Figure 5. Schematic diagram of plasmid pSC10.

Figure 6. Nucleotide sequence (SEQ ID NO:4) of the modified p7.5 promoter.

20 Figure 7. Schematic diagram of plasmid pSC59.

Figure 8. Schematic diagram of the HBV genome, illustrating the core and surface antigen-encoding regions.

25 Figure 9. Schematic diagram of plasmid pAM6.

Figure 10. Schematic diagram of plasmid pT7T318.

30 Figure 11. Schematic diagram of plasmid pRO-01. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

35 Figure 12. Schematic diagram of plasmid pRO-02. A restriction enzyme site shown in

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parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 13. Schematic diagram of plasmid
5 pRO-03.

Figure 14. Schematic diagram of plasmid
pRO-05. A restriction enzyme site shown in
parentheses means that the site was present in the
parental plasmid construct but was destroyed during
10 cloning procedures.

Figure 15. Schematic diagram of plasmid
pRO-06. A restriction enzyme site shown in
parentheses means that the site was present in the
parental plasmid construct but was destroyed during
15 cloning procedures.

Figure 16. Schematic diagram of plasmid
pT7T3/S. A restriction enzyme site shown in
parentheses means that the site was present in the
parental plasmid construct but was destroyed during
20 cloning procedures.

Figure 17. Schematic diagram of plasmid
pT7T3/S2.

Figure 18. Schematic diagram of plasmid
pLEH-01.

25 Figure 19. Schematic diagram of plasmid
pLEH-02. A restriction enzyme site shown in
parentheses means that the site was present in the
parental plasmid construct but was destroyed during
cloning procedures.

30 Figure 20. Schematic diagram of plasmid
pLEH-03. A restriction enzyme site shown in
parentheses means that the site was present in the
parental plasmid construct but was destroyed during
cloning procedures.

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Figure 21. Schematic diagram of plasmid pLEH-04. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 22. Nucleotide sequence (SEQ ID NO:5) and amino acid sequence (SEQ ID NO:6) of LS.

Figure 23. Nucleotide sequence (SEQ ID NO:7) and amino acid sequence (SEQ ID NO:8) of MS.

Figure 24. Nucleotide sequence (SEQ ID NO:9) and amino acid sequence (SEQ ID NO:10) of S.

Figure 25. Schematic diagram of plasmid pRO-09B. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 26. Schematic diagram of plasmid pT7T3/C. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 27. Schematic diagram of plasmid pT7T3/CHB.

Figure 28. Schematic diagram of plasmid pT7T3/CRB.

Figure 29. Schematic diagram of plasmid pT7T3/CODM.

Figure 30. Nucleotide sequence (SEQ ID NO:12) and amino acid sequence (SEQ ID NO:13) of coreΔ8.

Figure 31. Schematic diagram of plasmid pCRB/24. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 32. Schematic diagram of plasmid pCODM/24.

Figure 33. Nucleotide sequence (SEQ ID NO:14) and amino acid sequence (SEQ ID NO:15) of full-length core in plasmid pCODM/24.

Figure 34. Schematic diagram of plasmid pGS53X.

Figure 35. Schematic diagram of plasmid pGS53/S.

Figure 36. Schematic diagram of plasmid pGS53/S2.

Figure 37. Schematic diagram of plasmid pGS53/S1.

Figure 38. Schematic diagram of plasmid pHTL-8.

Figure 39. Schematic diagram of plasmid pHTL-9.

Figure 40. Schematic diagram of plasmid pHTL-10.

Figure 41. Schematic diagram of plasmid pHTL-10M.

Figure 42. Schematic diagram of plasmid pHTL-25. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 43. Schematic diagram of plasmid pHTL-26.

Figure 44. Nucleotide sequence (SEQ ID NO:25) and amino acid sequence (SEQ ID NO:26) of core-preS1*.

Figure 45. Schematic diagram of plasmid pHTL-27.

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Figure 46. Nucleotide sequence (SEQ ID NO:29) and amino acid sequence (SEQ ID NO:30) of core-pres2.

5 Figure 47. Schematic diagram of plasmid pHTL-28.

Figure 48. Nucleotide sequence (SEQ ID NO:33) and amino acid sequence (SEQ ID NO:34) of core-S*.

10 Figure 49. Schematic diagram of plasmid pSC10AlacZ.

Figure 50. Schematic diagram of plasmid pDPV. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

15 Figure 51. Schematic diagram of plasmid pDPV-01.

Figure 52. Schematic diagram of plasmid pRO-10.

20 Figure 53. Schematic diagram of plasmid pRO-16. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

25 Figure 54. Schematic diagram of plasmid pRO-11. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

30 Figure 55. Schematic diagram of plasmid pRO-17. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

35

Figure 56. Schematic diagram of plasmid pRO-22. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 57. Schematic diagram of plasmid pRO-12.

Figure 58. Schematic diagram of plasmid pRO-13B. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 59. Schematic diagram of plasmid pRO-18. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 60. Schematic diagram of plasmid pRO-19.

Figure 61. Schematic diagram of plasmid pRO-19/24. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 62. Schematic diagram of plasmid pHTL-5. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 63. Schematic diagram of plasmid pHTL-6.

Figure 64. Schematic diagram of plasmid pHTL-7.

Figure 65. Schematic diagram of plasmid pHTL-11.

Figure 66. Schematic diagram of plasmid pHTL-12.

Figure 67. Schematic diagram of plasmid pRO-16M. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 68. Schematic diagram of plasmid pHTL-30.

Figure 69. Schematic diagram of plasmid pHTL-13.

Figure 70. Schematic diagram of plasmid pHTL-15. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 71. Schematic diagram of plasmid pHTL-17. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 72. Schematic diagram of plasmid pHTL-33.

Figure 73. Schematic diagram of plasmid pHTL-34.

Figure 74. Schematic diagram of plasmid pHTL-35.

Figure 75. Schematic diagram of plasmid pHTL-36.

Figure 76. Schematic diagram of plasmid pPB-05. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 77. Schematic diagram of plasmid pPB-09.

Figure 78. Schematic diagram of plasmid pET-3d. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 79. Schematic diagram of plasmid pT7/core. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 80. Schematic diagram of plasmid pPB-04.

Figure 81. Nucleotide sequence (SEQ ID NO:44) and amino acid sequence (SEQ ID NO:45) of preS1-core Δ 8.

Figure 82. Schematic diagram of plasmid pRO-21. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 83. Nucleotide sequence (SEQ ID NO:48) and amino acid sequence (SEQ ID NO:49) of preS1-full-length core.

Figure 84. Schematic diagram of plasmid pRO-23. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 85. Schematic diagram of plasmid pHTL-23. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 86. Schematic diagram of plasmid pHTL-24. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during
5 cloning procedures.

Figure 87. Schematic diagram of plasmid pHTL-18. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during
10 cloning procedures.

Figure 88. Schematic diagram of plasmid pHTL-14. A restriction enzyme site shown in parentheses means that the site was present in the parental plasmid construct but was destroyed during
15 cloning procedures.

Figure 89. Schematic diagram of plasmid pHTL-31.

Figure 90. Schematic diagram of plasmid pHTL-32. A restriction enzyme site shown in
20 parentheses means that the site was present in the parental plasmid construct but was destroyed during cloning procedures.

Figure 91. A representative Western blot of polypeptides in cells infected by recombinant vaccinia
25 viruses, probed with anti-S antibodies. Lane A contains proteins isolated from nonrecombinant (wild-type) vaccinia virus. Lane B contains proteins from a recombinant virus which does not express any S-related antigens. Lanes C (pRO-18) and D (pGS53/S1)
30 are samples from recombinant viruses expressing the two forms of the LS antigen, nonglycosylated and glycosylated polypeptides of expected molecular weights 39 kD and 42 kD. Lanes E (pGS53/S) and F (pHTL-8) contain proteins from recombinant viruses
35 expressing the two forms of the S antigen, with

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nonglycosylated and glycosylated forms having expected molecular weights of 24 kD and 27 kD. Lanes G (pHTL-14), H (pGS53/S2) and I (pRO-23) contain proteins from recombinant viruses expressing the two forms of the MS antigen, with singly and doubly glycosylated forms of expected molecular weight 33 kD and 36 kD, respectively.

5. DETAILED DESCRIPTION OF THE INVENTION

10 The present invention provides recombinant vaccinia viruses which are capable of expressing a plurality of immunogenic HBV epitopes comprising at least one core antigen epitope, at least one surface antigen epitope, or any combination of the foregoing.

15 In one embodiment, a plurality of core and/or surface antigen epitopes is expressed. Core antigen epitopes are selected from the group consisting of wild-type core antigen, e antigen, and derivatives thereof. Surface antigen epitopes are those encoded by ORF S, and are selected from the group consisting of S, MS, LS, preS2, preS1, and derivatives thereof. "Epitope" as used herein refers to an antigenic determinant, i.e., an amino acid sequence that is capable of being immunospecifically bound by an antibody. Thus, for

20 example, a protein containing a core antigen epitope can be detected by observing the ability of such protein to be bound by an anti-core protein antibody.

25 ~~The core antigen derivatives provided by the invention are those derivatives (including but not limited to fragments) which display core antigen antigenicity, i.e., are capable of being bound by an anti-core antibody.~~ Similarly, the surface antigen derivatives provided by the invention are those derivatives (including but not limited to fragments) which display

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surface antigen antigenicity, i.e., are capable of being bound by an anti-surface antigen antibody.

In a specific embodiment, a combination of the foregoing core and/or surface antigen epitopes is expressed as a fusion protein in the vaccinia viruses of the invention. "Fusion protein," as used herein, refers to a protein comprising an amino acid sequence from a first protein covalently linked via a peptide bond at its carboxy terminus to the amino terminus of an amino acid sequence from a second, different protein.

In one embodiment, a vaccine formulation of the invention contains a single type of recombinant vaccinia virus of the invention. In another embodiment, a vaccine formulation comprises a mixture of two or more recombinant viruses of the invention. Preferred viruses contain plural HBV antigens including but not limited to a combination of one of S, MS, LS, and full-length core, coreΔ8 (see Section 6.1.2 *infra*), preS1-coreΔ8, preS1-complete core, core-preS1*, core-preS2, or core-S* (the asterisks denoting the presence of an immunogenic fragment of the preceding antigen; hyphens denoting a fusion protein).

In various embodiments, the core and/or surface antigen epitopes can be expressed by the same recombinant virus, under the control of different promoters active in vaccinia virus. In a preferred aspect, two divergently oriented promoters are used. In a specific embodiment, a recombinant vaccinia virus expresses a surface-core (written in the amino to carboxy-terminal order) or core-surface fusion protein (e.g., core-preS1, core-preS2, core-S, or preS1-core) under the control of a first promoter, and expresses a

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surface antigen (e.g., MS) under the control of a second promoter.

In another specific embodiment, a mixture of recombinant vaccinia viruses is provided, comprising a first virus capable of expressing core-preS1, a second virus capable of expressing core-preS2, and a third virus capable of expressing core-S. In another embodiment, such a mixture comprises a first virus capable of expressing core-preS1 or core-preS1*, a second virus capable of expressing core-preS2, and a third virus capable of expressing S. In another embodiment, such a mixture comprises a first virus capable of expressing core-preS1 or core-preS1*, and a second virus capable of expressing MS. In yet another embodiment, such a mixture comprises a first virus capable of expressing core-preS2, and a second virus capable of expressing S.

Other specific embodiments include the recombinant viruses disclosed in Section 6 *infra*.

The vaccine formulations of the present invention provide efficacious protection against HBV infection, because, as live viral vaccines, multiplication of the vaccine strain and expression of its HBV epitope(s) in the host leads to prolonged immune stimulus, and the combination of HBV immunogenic epitopes thereby expressed leads to protective immunity. The prolonged immune stimulus provided by the live viral vaccines of the invention is of similar kind and magnitude to that occurring in natural subclinical infections, and therefore, can confer substantial long-lasting immunity. The identity and structural context of the immunogenic epitopes expressed according to the invention provide protection against HBV infection. Thus, the present invention provides methods of prevention or treatment

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of HBV infection and its clinical manifestations (hepatitis, hepatoma) comprising administering one or more of the recombinant vaccinia viruses of the invention.

5 Furthermore, the vaccine formulations of the invention provide one or more of the following benefits: stability for long periods without refrigeration; ease of production; low cost of production; ability to be administered by local
10 workers without advanced medical training; and effectiveness in one dose. The vaccinia viruses which express an immunogenic fragment of more than one HBV protein cause immunological reactions against more components of HBV than can be presented by single
15 subunit vaccines.

5.1. DNA SEQUENCES ENCODING HBV EPITOPES

Any DNA sequence which encodes an immunogenic (capable of provoking an immune response)
20 HBV epitope, which produces protective immunity against hepatitis when expressed as a fusion or nonfusion protein in a recombinant vaccinia virus of the invention, alone or in combination with other HBV epitopes expressed by the same or a different vaccinia
25 virus recombinant, can be isolated for use in the vaccine formulations of the present invention.

In a specific embodiment, epitopes of HBV antigens can be identified by virtue of their hydrophilicity, by carrying out a hydrophilicity
30 analysis (Hopp and Woods, 1981, Proc. Natl. Acad. Sci. USA 78:3824) to generate a hydrophilicity profile. A hydrophilicity profile can be used to identify the hydrophobic and hydrophilic regions of a protein and the corresponding regions of the gene sequence which
35 encode such proteins.

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Preferred epitopes are those of the surface and core antigens described *supra*, specific embodiments of which are disclosed in examples section 6 herein (see also Table I). However, many different HBV surface and core antigen proteins or peptides can be expressed. These include but are not limited to naturally occurring membrane glycoproteins produced from recombinant vaccinia infected cells, which are glycosylated and may be transported to the cell surface. Peptides or proteins comprising surface antigen epitopes include but are not limited to an approximately 42,000 dalton glycoprotein consisting of preS1-preS2-S; an ~39,000 dalton unglycosylated protein consisting of preS1-preS2-S; an ~36,000 dalton glycoprotein (glycosylated at two sites) consisting of preS2-S; an ~33,000 dalton glycoprotein (glycosylated at one site) consisting of preS2-S; an ~27,000 dalton glycoprotein (glycosylated at one site) consisting of S; and an ~24,000 dalton unglycosylated protein consisting of S.

The immunogenic peptides and proteins expressed by the recombinant viruses of the invention can be secreted or not secreted by a host cell infected with the virus. Such proteins which are not secreted can be intracellular proteins or cell surface membrane proteins. In a preferred aspect, the HBV protein or peptide (containing the immunogenic epitope) expressed by the recombinant vaccinia virus is localized extracellularly (secreted) or is a cell surface protein. However, extracellular or cell surface localization is not required, since intracellular localization can also evoke an effective immune response (see, e.g., Brown et al., 1987, J. Inf. Disc. 155:86).

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The sequences encoding the immunogenic peptides or proteins are preferably present in single copies, but can also be present in multiple copies within the vaccinia virus genome. If multiple copies are present, care must be taken to ascertain that the recombinant virus stably maintains each of the multiple copies. In a preferred aspect, in an embodiment in which two copies are present, stability of the copies in the genome is maintained by localizing the individual copies relatively distant from each other in the genome with essential sequences between the copies, or, perhaps, by orienting the copies divergently. Stability of the copies in the genome can be confirmed by methods known in the art, e.g., Southern analysis. In a specific embodiment, multiple copies are avoided by employing, in the recombinant vaccinia viruses of the invention, HBV sequences which do not overlap by (i.e., do not contain an identical sequence of) more than 20 nucleotides, and preferably, do not overlap by more than 10 nucleotides. In a particular embodiment wherein a recombinant virus of the invention encodes a first and a second protein, each protein containing core and/or surface antigen epitopes, to maintain stability, the core and/or surface antigen sequences, or portions thereof displaying the antigenicity of such core and surface antigen sequences, respectively, in the first fusion protein are not present in the second fusion protein.

In a preferred aspect, the nucleotide sequence encoding the peptide or proteins comprising HBV immunogenic epitope(s) lacks introns, e.g., is a cDNA sequence, since any introns will not be spliced out. Thus, for example, no introns containing stop codons in the desired reading frame may be contained in the HBV-encoding nucleotide sequence. The

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nucleotide sequence preferably contains a ribosomal binding site, or is placed within an insertion vector (see Section 5.2) so as to be operatively linked to a ribosomal binding site.

- 5 The DNA sequence encoding the HBV epitope(s) can be obtained from any of numerous sources such as cloned HBV DNA, genomic HBV DNA, cDNA of HBV RNA, or chemically synthesized DNA (see, e.g., U.K. Patent Publication No. GB 2034323A-published-June-4, 1980;
10 Ganem and Varmus, 1987, Ann. Rev. Biochem. 56:651-693; Tiollais et al., 1985, Nature 317:489-495), and manipulated by recombinant DNA methodology well known in the art (see Sambrook et al., 1991, Molecular Cloning, A Laboratory Manual, 2d ed., Cold Spring
15 Harbor Laboratory Press, New York).

- Plasmid pAM6 contains the entire genome of HBV (subtype adw), and is available from the American Type Culture Collection (ATCC). In this plasmid, the HBV DNA has been inserted into the cloning vector
20 pBR322 at a BamHI restriction enzyme site within the preS2 region to allow replication of the DNA in *E. coli*. Thus, the MS and LS antigen open reading frames (ORFs) in pAM6 are interrupted. In order to express the MS and LS antigens, it is necessary to reunite the
25 surface antigen ORFs (e.g., as described in the examples sections *infra*).

- In order to generate HBV DNA fragments, the HBV DNA may be cleaved at specific sites using various restriction enzymes. Alternatively, one may use
30 DNaseI in the presence of manganese, or mung bean nuclease (McCutchan et al., 1984, Science 225:626), to fragment the DNA, or the DNA can be physically sheared, as for example, by sonication. The linear DNA fragments can then be separated according to size
35 by standard techniques, including, but not limited to,

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agarose and polyacrylamide gel electrophoresis and column chromatography.

Any restriction enzyme or combination of restriction enzymes may be used to generate HBV DNA fragment(s) containing the desired epitope(s), provided the enzymes do not destroy the immunopotency of the encoded product. Consequently, many restriction enzyme combinations may be used to generate DNA fragments which, when inserted into an appropriate vector, are capable of directing the production of the peptide containing the HBV epitope(s).

Once the DNA fragments are generated, identification of the specific DNA fragment containing the desired HBV sequence may be accomplished in a number of ways. For example, if a small amount of the desired DNA sequence or a homologous sequence is previously available, it can be used as a labeled probe (e.g., nick translated) to detect the DNA fragment containing the desired sequence, by nucleic acid hybridization. Alternatively, if the sequence of the derived gene or gene fragment is known, isolated fragments or portions thereof can be sequenced by methods known in the art, and identified by a comparison of the derived sequence to that of the known DNA or protein sequence. Alternatively, the desired fragment can be identified by techniques including but not limited to mRNA selection, making cDNA to the identified mRNA, chemically synthesizing the gene sequence (provided the sequence is known), or selection on the basis of expression of the encoded protein (e.g., by antibody binding) after "shotgun cloning" of various DNA fragments into an expression system.

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The sequences encoding HBV peptides to be expressed in recombinant vaccinia viruses according to the present invention, whether produced by recombinant DNA methods, chemical synthesis, or purification techniques, include but are not limited to sequences encoding all or part (fragments) of the amino acid sequences of HBV-specific antigens, as well as other derivatives and analogs thereof. In a specific embodiment, the derivative or analog is functionally active, i.e., capable of exhibiting one or more functional activities associated with a full-length, wild-type HBV antigen (e.g., core or surface antigen). In a preferred embodiment, such derivatives or analogs which have the desired immunogenicity or antigenicity (capable of being bound by an antibody to the HBV antigen) can be encoded. In another specific embodiment, a surface antigen derivative which retains the ability to assemble into 22 nm particles is encoded. In yet another specific embodiment, a core antigen derivative which retains the ability to assemble into core particles (see, e.g., Cohen and Richmond, 1982, Nature 296:677-678) is encoded. In yet another embodiment, core and/or surface antigen derivatives which retain the ability to assemble into viral particles are encoded. Derivatives or analogs of HBV antigens can be tested for the desired activity by procedures known in the art, including but not limited to standard immunoassays.

In particular, HBV antigen derivatives can be made by altering the encoding HBV antigen nucleotide sequences by substitutions, additions or deletions that provide for functionally equivalent molecules. Due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially the same amino acid sequence as a native

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HBV gene or portion thereof may be used in the practice of the present invention. These include but are not limited to nucleotide sequences comprising all or portions of HBV genes or cDNAs which are altered by the substitution of different codons that encode a functionally equivalent amino acid residue within the sequence, thus producing a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine, and histidine. The negatively charged (acidic) amino acids include aspartic and glutamic acid.

Derivatives or analogs of HBV antigens include but are not limited to those peptides which are substantially homologous to an HBV antigen or fragments thereof, or whose encoding nucleic acid is capable of hybridizing to an HBV antigen-encoding nucleic acid sequence, e.g., under conditions of high stringency (e.g., 0.1 X SSC, 65°C).

The HBV antigen derivatives and analogs can be produced by various methods known in the art. For example, a cloned HBV gene sequence can be modified by any of numerous strategies known in the art (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory, Cold Spring

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Harbor, New York). The sequence can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated *in vitro*. In the production of
5 the gene encoding a derivative or analog of an HBV antigen, care should be taken to ensure that the modified gene remains within the same translational reading frame as the antigen, uninterrupted by translational stop signals, in the gene region where
10 the desired HBV epitope(s) are encoded.

Additionally, the HBV antigen-encoding nucleic acid sequence can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination sequences, or to create
15 variations in coding regions and/or form new restriction endonuclease sites or destroy preexisting ones, to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used, including but not limited to, *in vitro* site-
20 directed mutagenesis (Hutchinson, C., et al., 1978, J. Biol. Chem 253:6551), use of TAB® linkers (Pharmacia), etc.

In another specific embodiment, the encoded HBV antigen derivative is a chimeric, or fusion,
25 protein comprising an HBV protein or fragment thereof fused to a non-HBV amino acid sequence. Such a chimeric protein is encoded by a nucleic acid encoding the HBV coding sequence joined in-frame to a non-HBV coding sequence. Such a chimeric product can be made
30 by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame.

A DNA sequence encoding an HBV epitope which
35 is a hapten, i.e., a molecule that is antigenic in

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that it can react selectively with cognate antibodies, but not immunogenic in that it cannot elicit an immune response when administered without adjuvants or carrier proteins, can be isolated for use in the vaccine formulations of the present invention, since it is envisioned that, in particular embodiments, presentation by the vaccinia viruses of the invention can confer immunogenicity to the hapten expressed by the virus.

Once identified and isolated, the HBV DNA containing the sequence(s) of interest is then inserted into a recombinant vaccinia virus such that it can be expressed by such virus. Preferably, this is accomplished by first inserting the HBV DNA into a plasmid vector which is capable of subsequent transfer to a vaccinia virus genome by homologous recombination. (see Section 5.2 *infra*).

5.2. CONSTRUCTION OF INSERTION VECTORS
CONTAINING SEQUENCES WHICH ENCODE
HBV SURFACE AND/OR CORE EPITOPE(S)

In a preferred aspect of the invention for constructing the recombinant vaccinia viruses, the desired DNA sequence encoding the HBV epitope(s) is inserted, using recombinant DNA methodology (see Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York) into an insertion (preferably, plasmid) vector flanked by (preferably) nonessential vaccinia DNA sequences, thus providing for subsequent transfer of its chimeric gene(s) into vaccinia virus by homologous recombination. The HBV sequences are placed in the vector such that they can be expressed under the control of a promoter functional in vaccinia virus.

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Expression of foreign DNA in recombinant vaccinia viruses requires the positioning of promoters functional in vaccinia so as to direct the expression of the protein-coding HBV DNA sequences. Plasmid insertion vectors have been constructed to insert chimeric genes into vaccinia virus. One type of plasmid insertion vector is composed of: (a) a vaccinia virus promoter including the transcriptional initiation site; (b) one or more unique restriction endonuclease cloning sites located downstream from the transcriptional start site for insertion of foreign DNA fragments; (c) nonessential vaccinia virus DNA (such as the thymidine kinase (TK) gene) flanking the promoter and cloning sites which directs insertion of the chimeric gene into the homologous nonessential region of the virus genome; and (d) a bacterial origin of replication and antibiotic resistance marker for replication and selection in *E. coli*. Examples of such vectors are described by Mackett (Mackett et al., 1984, *J. Virol.* 49:857-864). The DNA encoding HBV epitope(s) is inserted into a suitable restriction endonuclease cloning site (b, above). Various derivatives of this prototype insertion vector can also be used, e.g., with multiple restriction sites, with the β -galactosidase gene (*lacZ*) to allow selection of plaques by color, with inducible gene expression (e.g., by inclusion of a bacterial *lac* repressor system), etc. (see, e.g., Boyle et al., 1985, *Gene* 35:169-177; Chakrabarti et al., 1985, *Mol. Cell. Biol.* 5:3403-3409; Falkner et al., 1988, *J. Virol.* 62:1849-1854; Falkner et al., 1987, *Nucl. Acids Res.* 15:7192; Franke et al., 1985, *Mol. Cell. Biol.* 5:1918-1924; Panicali et al., 1986, *Gene* 47:193-199; Patel et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:9431-9435; Fuerst et al., 1989, *Proc. Natl. Acad.*

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Sci. USA 86:2549-2553). In addition to plasmid insertion vectors, insertion vectors based on single-stranded M13 bacteriophage DNA (Wilson et al., 1986, Gene 49:207-213) can be used.

5 The inserted HBV DNA should preferably not contain introns since intron sequences will not be removed during the viral life cycle, and insertion should preferably be so as to place the HBV coding sequences in close proximity to the promoter, with no
10 other start codons in between the initiator ATG and the 5' end of the transcript.

 Preferably, a plasmid insertion vector such as described *supra*, with a convenient restriction site for insertion of the HBV DNA, is used. Alternatively,
15 if the complementary restriction sites used to fragment the HBV DNA are not present in the cloning vector, the ends of the DNA molecules may be modified. Such modifications include producing blunt ends by digesting back single-stranded DNA termini or by
20 filling the single-stranded termini so that the ends can be blunt-end ligated. Alternatively, any site desired may be produced by ligating nucleotide sequences (linkers) onto the DNA termini; these ligated linkers may comprise specific chemically
25 synthesized oligonucleotides encoding restriction site recognition sequences. Other methods known in the art may be used.

 The plasmid insertion vector should contain transcriptional and translational regulatory elements
30 that are active in vaccinia virus. High expression levels in the derived recombinant virus can be obtained by using strong promoters or, less preferably, by inserting multiple copies of a single HBV sequence. In the use of multiple copies, care
35 should be taken to confirm stable maintenance of the

copies in the vaccinia virus genome (see discussion *supra*).

As mentioned *supra*, the plasmid should be configured so that the HBV sequences are under the control of a promoter active in vaccinia virus. Such a promoter can be a native vaccinia promoter or a non-native promoter active in vaccinia virus. The promoter can be natural or synthetic. The plasmid can contain more than one promoter, each directing the expression of a different sequence encoding HBV epitope(s). In a preferred aspect, two such divergently oriented promoters are used. Promoters which can be used in the insertion vectors include but are not limited to the vaccinia virus thymidine kinase (TK) promoter, the 7.5K promoter (termed herein "p7.5"), a modified p7.5 (see *infra*), the 11K promoter (termed herein "p11"), the F promoter (Paoletti et al., 1984, Proc. Natl. Acad. Sci. USA 81:193-197), and various early and late vaccinia promoters (see Moss, 1990, *Virology*, 2d ed., ch. 74, Fields et al., eds., Raven Press, Ltd., New York, pp. 2079-2111). In the use of a native vaccinia virus promoter, a promoter active both early and late in the viral life cycle is preferred.

In a specific embodiment, the plasmid insertion vector contains (for eventual transfer into vaccinia virus) a T7 RNA polymerase coding sequence under the control of a promoter active in vaccinia virus, and the HBV coding sequences under the control of the T7 promoter. In another specific embodiment, a plasmid insertion vector contains a co-expression system consisting of divergently oriented promoters, one directing transcription of the HBV sequences, the other directing transcription of a reporter gene or selectable marker, to facilitate detection or

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selection of the eventual recombinant vaccinia virus (see, e.g., Fuerst et al., 1987, Mol. Cell. Biol. 5:1918-1924). In preferred aspects, the p7.5, p11, or modified versions thereof are employed, some of which
5 are described in more detail below.

A strong vaccinia promoter, denoted here as "p7.5" (Cochran et al., 1985, J. Virol. 54:30-37), having the sequence provided in Figure 2 (SEQ ID NO:2), can be one of several vaccinia or vaccinia-like
10 promoters used to direct expression of the HBV sequences. The p7.5 promoter is so named because it normally directs expression of a vaccinia polypeptide of 7.5 kilodaltons molecular weight. The transition from early to late events in viral replication is
15 generally considered to be marked by the onset of viral DNA replication, and p7.5 contains elements which are active both early and late in viral replication, making it act as a constitutive promoter. Promoter p7.5 is contained in plasmid pGS53 (Fig. 3)
20 (Chakrabarti et al., 1985, Mol. Cell. Biol. 5:3403-3409; kindly provided by Dr. Bernard Moss, National Institutes of Health). This plasmid contains fragments of the vaccinia thymidine kinase (TK) gene positioned so as to facilitate homologous
25 recombination of the plasmid into that site in the vaccinia genome.

Another vaccinia promoter, p11, in nature directs expression of a vaccinia structural protein of 11 kilodaltons (European patent application 0198328,
30 Hoffman LaRoche). p11, unlike the p7.5 promoter, is active only late in viral replication. The nucleotide sequence of p11 is shown in Figure 4 (SEQ ID NO:3). As described in Example 6, *infra*, a number of constructs were made using this promoter, both alone
35 and in combination with p7.5, to direct expression of

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HBV antigens. The 11 kD promoter is contained in a plasmid called pSC10 (Fig. 5, Chakrabarti et al., *supra*; kindly provided by Dr. Bernard Moss), which contains the gene coding for the bacterial enzyme β -galactosidase, *lacZ*, located downstream of the p11 promoter. In a specific embodiment, a p11- β -gal cassette is inserted into the middle of the vaccinia TK gene so that this expression unit can be inserted by *in vivo* recombination into the TK gene in the virus.

A strong vaccinia-like promoter used to direct expression of the hepatitis B antigens, termed herein "modified p7.5" has the nucleotide sequence set forth in Figure 6 (SEQ ID NO:4). The modified p7.5 promoter (constructed in the laboratory of Dr. Bernard Moss) is a strong synthetic promoter that is active both early and late in viral replication. The modified p7.5 promoter has a sequence based partly on the sequence of the p7.5 promoter. The modified p7.5 promoter is contained in plasmid pSC59 (Fig. 7; kindly provided by Dr. Bernard Moss).

Specific initiation signals are also required for efficient translation of inserted protein coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where the entire HBV gene including its own initiation codon and adjacent sequences are inserted into the appropriate vectors, no additional translational control signals may be needed. However, in cases where only a portion of the gene sequence is inserted, exogenous translational control signals, including the ATG initiation codon, must be provided. The initiation codon must furthermore be in phase with the reading frame of the protein coding sequences to ensure translation of the entire insert. These

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exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic.

In a preferred embodiment, the ATG
5 initiation codon of the HBV antigen or portion thereof is "upregulated," i.e., contains a sequence upstream of that encoding the initiator methionine that matches a consensus sequence associated with strong ribosome binding. In a specific embodiment, the ATG codon of
10 MS is upregulated.

As described *supra*, the plasmid insertion vector contains at least one set of HBV coding sequences operatively linked to a promoter, flanked by sequences preferably nonessential for vaccinia viral
15 replication. Such nonessential sequences include but are not limited to the TK gene (Mackett et al., 1984, J. Virol. 49:857-864), the vaccinia HindIII-F DNA fragment (Paoletti et al., 1984, Proc. Natl. Acad. Sci. USA 81:193-197), the vaccinia growth factor gene
20 situated within both terminal repeats (Buller et al., 1988, J. Virol. 62:866-874), the N2 and M1 genes (Tamin et al., 1988, Virology 165:141-150), the M1 subunit of the ribonucleotide reductase gene in the vaccinia HindIII-I DNA fragment (Child et al., 1990, Virology 174:625-629), the vaccinia hemagglutinin
25 (Shida et al., 1988, J. Virol. 62:4474-4480), vaccinia 14 kD fusion protein gene (Rodriguez et al., 1989, Proc. Natl. Acad. Sci. USA 86:1287-1291), etc. (see also Buller and Palumbo, 1991, Microbiol. Rev.
30 55(1):80-122). TK sequences are preferred for use; use of such sequences results in the generation of TK⁻ recombinant viruses. TK⁻ recombinants have been shown to be attenuated relative to the parent strain (Buller et al., 1985, Vaccines 85:163), which may be an

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advantage from a safety standpoint in the development of new vaccinia-based vaccines.

In an alternative embodiment, because vaccinia recombinants containing HBV sequences within
5 coding regions such as TK may be overly attenuated, the HBV-encoding sequences are inserted into a region of the vaccinia genome that does not encode protein, e.g., an intergenic region. In addition, insertion into such a non-coding region in conjunction with
10 insertion into a nonessential coding region such as TK might enable the generation of recombinant vaccinia viruses with multiple insertions which are no more attenuated than those viruses with a single insertion only in a nonessential coding region. The strategy
15 for choosing a non-coding region is based on several parameters, one of which is the length of the region, i.e., the distance between surrounding genes. A larger distance is preferable to a smaller distance in order to avoid regulatory regions necessary for the
20 expression of surrounding genes. Another parameter is the function of the surrounding genes, nonessential genes being preferable to essential genes. A sequence and map of the wild-type vaccinia Copenhagen strain is found in Goebel et al., 1990, Virology 179:247-266.
25 For strains which have not been sequenced, the sequence of the chosen non-coding region is obtained or determined according to conventional nucleotide sequence techniques.

By way of example but not limitation,
30 construction of an insertion vector with intergenic flanking regions can be carried out as follows:

After an intergenic region is selected as a candidate nonessential non-coding region for insertion of foreign DNA, a pair of polymerase chain reaction
35 (PCR) primers having nucleotide sequences

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corresponding to a sequence within the chosen intergenic region is synthesized or obtained commercially. Primers are preferably chosen such that there is between 100 and 300 nucleotides between primers of a pair. 300 nucleotides has been designated herein as an upper length limit because the largest known non-coding region in the Copenhagen strain is approximately 400 nucleotides in length. In order to avoid potential regions of control of surrounding genes, it is preferable to leave a minimum of 50 nucleotides untouched on either side of the insertion region. Longer DNA sequences can also be amplified if primers hybridizing within the surrounding genes are used. Primers are designed so as to hybridize to complementary strands and allow amplification of the region between them. To facilitate later cloning, it is desirable to build a convenient restriction site into the primer sequence. Examples of sets of primers which may be used for the following non-coding regions, along with convenient restriction sites, are as follows.

TABLE I.

Non-coding Region	Primers	SEQ ID NO:	SITE
F14L-F15L	5'GTTGGTAGAATTCCAATTAT3'	50	EcoRI
	5'AAGAATGATCGATACAGTTT3'	51	Clal
C12L-C11R	5'GTACCCCGAATTCATACTTA3'	52	EcoRI
	5'AATAATATATCGATAATTGT3'	53	Clal
A53R-A55R	5'GTTGGAATTCGCTACTGAT3'	54	EcoRI
	5'TAACCAAGTATCGATATAAT3'	55	Clal

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Viral DNA is isolated from the wild type, e.g., Wyeth virus according to known procedures. The primers are then hybridized to the viral DNA under non-denaturing conditions. PCR (see Section 5.3) is then performed on the isolated DNA using the pair of primers corresponding to the chosen intergenic region. The amplified DNA is then digested with restriction enzymes which cut within the primer sequences and the resulting fragment is gel purified. The gel purified DNA is cloned into an appropriate vector using standard cloning techniques.

The cloned non-coding region is digested with a restriction enzyme at a site within the non-coding region. Noncoding regions which can potentially be used, with their approximate size and a convenient restriction site for insertion, are set forth in Table 2.

20

TABLE 2

25

Non-coding Region	Approximate Band Size of Non-coding Region	Internal Restriction Site
F14L-F15L	210 bp	SnaBI
C12L-C11R	260 bp	BclI
A53R-A55R	240 bp	SnaBI

30

In order to clone the desired HBV sequences downstream of vaccinia promoters in the vector, the desired promoter/HBV DNA construct is inserted within the cloned non-coding region using the appropriate restriction enzymes and sites. Preferably, the HBV sequences are inserted so as to be flanked by at least

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about 100 bp of the noncoding vaccinia DNA. Most preferably the sequences are inserted into the vector so as to be surrounded by about 500 bp of vaccinia DNA on each side, which may include some DNA from
5 nonessential vaccinia genes.

5.3. CONSTRUCTION AND IDENTIFICATION OF
RECOMBINANT VACCINIA VIRUSES
ENCODING HBV EPTOPE(S)

Recombinant vaccinia viruses are preferably
10 produced by transfection of the recombinant insertion
vectors containing the HBV sequences into cells
previously infected with vaccinia virus.
Alternatively, transfection can take place prior to
infection with vaccinia virus. Homologous
15 recombination takes place within the infected cells
and results in the insertion of the foreign gene into
the viral genome, in the region corresponding to the
insertion vector flanking regions. The infected cells
can be screened using a variety of procedures such as
20 immunological techniques, DNA plaque hybridization, or
genetic selection for recombinant viruses which
subsequently can be isolated. These vaccinia
recombinants preferably retain their essential
functions and infectivity and can be constructed to
25 accommodate up to approximately 35 kilobases of
foreign DNA.

Transfections may be performed by procedures
known in the art, for example, a calcium
chloride-mediated procedure (Mackett et al., 1985, The
30 construction and characterization of vaccinia virus
recombinants expressing foreign genes, in *DNA Cloning*,
Vol. II, Rickwood and Hames (eds.), IRL Press,
Oxford-Washington, D.C.) or a liposome-mediated
procedure (Rose et al., 1991, *Biotechniques*
35 10:520-525).

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Where, as is preferred, flanking TK sequences are used to promote homologous recombination, the resulting recombinant viruses thus have a disrupted TK region, permitting them to grow on a TK⁻ host cell line such as Rat2 (ATCC Accession No. CRL 1764) in the presence of 5-bromo-2'-deoxyuridine (BUDR), under which conditions non-recombinant (TK⁺) viruses will not grow. TK⁻ recombinants have been shown to be attenuated relative to the parent strain (Buller et al., 1985, *Infectious vaccinia virus TK⁻ recombinants that express foreign genes are less virulent than wild-type virus in mice*, in *Vaccines 85, Molecular and Chemical Basis of Resistance to Parasitic, Bacterial and Viral Disease*, R.A. Lerner, Chanock, R.M., and Brown, F. (eds.), Cold Spring Harbor Laboratory, New York, pp. 163-167), which may be an advantage from a safety standpoint in the development of new vaccinia-based vaccines.

In another embodiment, recombinant vaccinia viruses of the invention are made by *in vitro* cloning, and then packaging with a poxvirus sensitive to a selection condition, rather than by homologous recombination. For example, the HBV DNA sequences can be inserted into vaccinia genomic DNA using standard recombinant DNA techniques *in vitro*; this recombinant DNA can then be packaged in the presence of a "helper" poxvirus such as a temperature sensitive vaccinia virus mutant or a fowlpox virus which can be selected against under the appropriate conditions.

Various vaccinia virus strains known in the art can be used to generate the recombinant viruses of the invention. Characterized strains of low virulence are preferred. A preferred vaccinia virus is the New York City Department of Health Laboratories strain, prepared by Wyeth (available from the American Type

Culture Collection (ATCC), Accession No. VR-325).

Other vaccinia strains include but are not limited to the Elstree and Moscow strains, the strain of Rivers (CV-1 and CV-2), and the LC16m8 strain of Hashizume.

5 Selection of the recombinant vaccinia virus can be by any method known in the art, including hybridization techniques (e.g., using HBV DNA sequences as a hybridization probe), immunological techniques (e.g., assay for binding to antibodies
10 recognizing the encoded HBV epitope(s)), etc. In a preferred aspect where TK flanking sequences are used in the insertion vector, selection is for TK⁻ recombinants, as described above; screening for the correct recombinant is then carried out by molecular
15 analyses as described *infra*. In many preferred aspects, the method of choice for selection is dictated by the choice of insertion vector used to generate the recombinant viruses. For example, if a coexpression system vector is used, containing a
20 reporter gene or selectable marker, detection of recombinants is carried out by screening for the reporter gene expression or selecting for selectable marker expression. In an embodiment where the *lacZ* gene is incorporated, color screening methods known in
25 the order can be used to detect expression of β -galactosidase. Incorporation of neomycin or gpt genes allows selection by antibiotic resistance. Plaque size can also be used for screening. Many other methods will be known to the skilled artisan and
30 can be used.

 The selected recombinant vaccinia virus is then generally plaque-purified (preferably by at least three rounds of purification from a single viral plaque), and subjected to molecular analyses to verify
35 its identity and purity. Preferably, two types of

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molecular analyses are carried out: (i) nucleic acid analyses; and (ii) assays for expression of the encoded HBV epitope(s).

- For nucleic acid analyses, to verify that
- 5 the recombinant vaccinia virus contains the DNA sequences encoding HBV epitope(s), hybridization assays are preferably carried out using a labelled nucleic acid containing HBV sequences as a hybridization probe. For example, plaque-lift
- 10 hybridizations (see Mackett et al., 1985, in *DNA Cloning*, Vol. II, Rickwood and Hames (eds.), IRL Press, Oxford-Washington, D.C.), Southern hybridizations (Southern, 1975, *J. Mol. Biol.* 98:503-517; see Section 8.1. *infra*), and Northern
- 15 hybridizations (Freeman et al., 1983, *Proc. Natl. Acad. Sci. USA* 80:4094-4098) can be carried out. Other methods of nucleic acid analysis which can be employed are restriction endonuclease mapping (Sambrook et al., 1991, *Molecular Cloning*, A
- 20 Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory Press, New York), and DNA sequence analysis (e.g., according to Maxam and Gilbert, 1980, *Meth. Enzymol.* 65:499-560; Sanger et al., 1977, *Proc. Natl. Acad. Sci. USA* 74:5463; or Tabor and Richardson, U.S.
- 25 Patent No. 4,795,699; or by use of an automated DNA sequenator). If desired, polymerase chain reaction (PCR; U.S. Patent Nos. 4,683,202, 4,683,195 and 4,889,818; Gyllenstein et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:7652-7656; Ochman et al., 1988, *Genetics*
- 30 120:621-623; Loh et al., 1989, *Science* 243:217-220) can be done prior to sequencing in order to amplify the region of interest.

Southern blot hybridization can also be carried out using a hybridization probe containing the

35 desired vaccinia sequences to ensure that the HBV

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sequences have been inserted into the desired region of the vaccinia genome.

Protein analyses, to confirm expression of the encoded HBV epitope(s) by the selected recombinant vaccinia virus, can be carried out by any method known in the art, including functional or immunological assays, and are preferably accomplished by immunoassay methods employing antibodies to the encoded HBV epitope(s). Various immunoassays known in the art can be used, including but not limited to competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, *in situ* immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, immunoprecipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labelled. Many means are known in the art for detecting binding in an immunoassay and are envisioned for use.

In specific embodiments, western blot analyses can be carried out as described in Section 8.2. *infra*. ELISA can be carried out as described in Section 8.3 *infra*. Several immunoassays for HBV S or e antigens are commercially available (Abbott Laboratories, No. Chicago, IL).

Recombinant viruses containing a combination of epitopes from core and surface elements are a preferred embodiment of the invention and can be generated using the plasmids described in the examples
5 sections *infra*, and homologous recombination.

5.4. DETERMINATION OF VACCINE EFFICACY

Immunopotency of the HBV epitope(s) in their live vaccinia vaccine formulation can be determined by
10 monitoring the immune response of test animals following immunization with the recombinant vaccinia virus(es) expressing the HBV epitope(s). Generation of a humoral response may be taken as an indication of a generalized immune response, other components of
15 which, particularly cell-mediated immunity, may be important for protection against HBV. Test animals may include mice, rabbits, chimpanzees and eventually human subjects. HBV can be made to infect chimpanzees experimentally, although they do not develop chronic
20 infections. However, since chimpanzees are a protected species, the antibody response to an HBV vaccine of the invention can first be studied in a number of smaller, less expensive animals, with the goal of finding one or two best candidate viruses or
25 best combinations of viruses to use in chimpanzee efficacy studies.

Methods of introduction of the vaccine may include oral, intracerebral, intradermal, intramuscular, intraperitoneal, intravenous,
30 subcutaneous, intranasal or any other standard routes of immunization. The immune response of the test subjects can be analyzed by various approaches such as: the reactivity of the resultant immune serum to HBV antigens, as assayed by known techniques, e.g.,
35 enzyme linked immunosorbent assay (ELISA),

immunoblots, radioimmunoprecipitations, etc.; or protection from HBV infection and/or attenuation of hepatitis symptoms in immunized hosts.

In a specific embodiment, recombinant
5 vaccinia virus vaccines of the invention can be prepared in large quantities for animal studies. By way of example, this is done by infecting roller bottles containing 10^8 to 10^9 cells with virus, and harvesting after several days of infection. The cells
10 are pelleted, washed, and then disrupted by resuspension and homogenization in a hypotonic buffer. Nuclei and cellular debris are then pelleted and the virus-containing supernatant is sonicated to break up any virus aggregates. The viruses are then pelleted
15 through a cushion of 36% sucrose in a hard spin, followed by banding in a 24-40% sucrose gradient. The purified virus is then harvested by a hard spin, resuspended in a small volume, and titrated to determine viral concentration and yield. This process
20 may be scaled up using a tangential flow filtration apparatus, and a continuous flow homogenizer.

As one example of suitable animal testing, HBV vaccines of the invention may be tested in rabbits for the ability to induce an antibody response to HBV
25 antigens. Male specific-pathogen-free (SPF) young adult New Zealand White rabbits may be used. The test group of rabbits each receives approximately 5×10^8 pfu (plaque forming units) of the vaccine. A control group of rabbits receives an injection in 1 mM
30 Tris-HCl pH 9.0 of the parental non-recombinant vaccinia virus or of a recombinant virus which does not express HBV antigens.

Blood samples may be drawn from the rabbits every one or two weeks, and serum analyzed for
35 antibodies to the HBV antigens using, e.g., a

radioimmunoassay (Abbott Laboratories). The presence of antibodies specific for core protein or the surface antigens may be assayed using an ELISA. The sera may also be analyzed for antibodies to vaccinia, e.g., in
5 an enzyme-linked immunoassay. Because rabbits may give a variable response due to their outbred nature, it may also be useful to test the vaccines in mice.

Mice respond differently to HBV antigens depending on their H-2 (histocompatibility) type
10 (Milich and Chisari, 1982, J. Immunol. 129:320-325). Because there is little information available regarding the expression of HBV antigens from recombinant vaccinia viruses in mice, an HBV-responsive strain of mouse must be chosen, and an
15 appropriate dose of vaccinia virus must be administered to render the mouse strain responsive to recombinant viruses of the invention (see Section 8.4, *infra*).

Patas monkeys may be used to test for
20 immunogenicity of HBV vaccine formulation, although challenge experiments cannot be carried out since they are resistant to HBV infection. Chimpanzees may be tested for HBV vaccine efficacy (e.g., challenge experiments), since they can be infected by the virus.
25 In a specific embodiment, monkeys each receive intradermally approximately 5×10^8 pfu of recombinant Wyeth virus. A control monkey receives Wyeth (control) virus intradermally. Blood is drawn weekly for 12 weeks, and serum is analyzed for antibodies to
30 vaccinia, core, and S.

5.5. VACCINE FORMULATION AND ADMINISTRATION

The purpose of this embodiment of the invention is to formulate a vaccine in which the
35 immunogen is one or several recombinant vaccinia

virus(es) that express(es) HBV epitope(s) so as to elicit a protective immune (humoral and/or cell mediated) response against HBV infections for the prevention of hepatitis, hepatoma and/or other
5 undesirable correlates of HBV infection.

Many methods may be used to introduce the vaccine formulations of the invention; these include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous,
10 subcutaneous, intranasal routes, and via scarification (scratching through the top layers of skin, e.g., using a bifurcated needle). In a preferred embodiment, scarification is employed; intravenous administration is disfavored, since it is preferred to
15 have the virus replicate in the skin and not spread systemically.

The vaccine formulations of the invention comprise the recombinant vaccinia virus and a pharmaceutically acceptable carrier or excipient. The
20 recombinant virus can be replicating or nonreplicating, although replicating is preferred. Similarly, an enveloped virus is preferred over the non-enveloped form. Pharmaceutically acceptable carriers include but are not limited to saline,
25 buffered saline, dextrose, water, glycerol, sterile isotonic aqueous buffer, and combinations thereof. The formulation should suit the mode of administration.

The composition, if desired, can also
30 contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. Oral formulation can include standard
35 carriers such as pharmaceutical grades of mannitol,

lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc.

Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is administered by injection, an ampoule of sterile diluent can be provided so that the ingredients may be mixed prior to administration.

In a specific embodiment, the lyophilized recombinant vaccinia virus of the invention is provided in a first container; a second container comprises diluent consisting of an aqueous solution of 50% glycerin, 0.25% phenol, and an antiseptic (e.g., 0.005% brilliant green).

The precise dose of virus to be employed in the formulation will also depend on the route of administration, and the nature of the patient, and should be decided according to the judgment of the practitioner and each patient's circumstances according to standard clinical techniques. However, a suitable dosage range for administration via scarification with a bifurcated needle is 10^6 to 10^9 pfu/ml (see, e.g., Cooney et al., 1991, The Lancet 337:567-572, regarding recombinant vaccinia viruses expressing HIV proteins). Boosting is possible but not preferred. If boosting is desired, it may be preferable to boost with the HBV antigen in purified form rather than using a recombinant virus of the invention, since long-lasting immunity to vaccinia virus may limit the utility of recombinant vaccinia virus for repetitive boosting (see *id.*). Effective

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doses may also be extrapolated from dose-response curves derived from animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled
5 with one or more of the ingredients of the vaccine formulations of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products,
10 which notice reflects approval by the agency of manufacture, use or sale for human administration.

5.6. USE OF ANTI-HBV ANTIBODIES
GENERATED BY THE VACCINES
OF THE INVENTION

15 The antibodies generated against HBV by immunization with the recombinant viruses of the present invention also have potential uses in diagnostic immunoassays, passive immunotherapy, and generation of antiidiotypic antibodies.

20 The generated antibodies may be isolated by standard techniques known in the art (e.g., immunoaffinity chromatography, centrifugation, precipitation, etc.) and used in diagnostic immunoassays. The antibodies may also be used to
25 monitor treatment and/or disease progression. Any immunoassay system known in the art, such as those listed *supra*, may be used for this purpose including but not limited to competitive and noncompetitive assay systems using techniques such as
30 radioimmunoassays, ELISA (enzyme-linked immunosorbent assays), "sandwich" immunoassays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays,
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fluorescent immunoassays, protein A immunoassays and immunoelectrophoresis assays, to name but a few.

The vaccine formulations of the present invention can also be used to produce antibodies for
5 use in passive immunotherapy, in which short-term protection of a host is achieved by the administration of pre-formed antibody directed against a heterologous organism (in this case, HBV).

The antibodies generated by the vaccine
10 formulations of the present invention can also be used in the production of antiidiotypic antibody. The antiidiotypic antibody can then in turn be used for immunization, in order to produce a subpopulation of antibodies that bind the initial antigen of the
15 pathogenic microorganism (Jerne, 1974, Ann. Immunol. (Paris) 125c:373; Jerne, et al., 1982, EMBO J. 1:234).

5.7. THERAPEUTIC USE OF THE RECOMBINANT VACCINIA VIRUSES OF THE INVENTION

In this embodiment, the recombinant vaccinia
20 viruses of the invention, encoding HBV immunogenic epitope(s), are administered therapeutically, for the treatment of hepatitis or other undesirable correlates of HBV infection. Administration of such viruses,
25 e.g., to neonates and other human subjects, can be used as a method of immunostimulation, to boost the host's immune system, enhancing cell-mediated and/or humoral immunity, and facilitating the clearance of HBV. The viruses of the invention can be administered
30 alone or in combination with other anti-viral therapies, including but not limited to α -interferon and vidarabine phosphate.

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6. CONSTRUCTION OF VECTORS ENCODING HBV EPITOPES

Some of the vectors which were constructed to contain DNA sequences encoding HBV surface antigen and/or core epitopes, under the control of a promoter functional in vaccinia virus, are listed in Table 3, along with their encoded antigens and the promoters operably linked to the HBV DNA. These vectors and their construction are described in the subsections below.

TABLE 3

Plasmids Containing Sequences Encoding
HBV Epitopes Under the Control of a
Promoter Functional in Vaccinia Virus

PLASMID	PROMOTER		
	p7.5	p11	modified p7.5
pSC10		β -galactosidase	
pGS53/S	S		
pGS53/S2	MS		
pGS53/S1	LS		
pHTL-5		core(full-length)	
pHTL-6		core(full-length)	S
pHTL-7		core(full-length)	LS
pHTL-8			S
pHTL-9			LS
pHTL-10			MS
pHTL-10M			MS (upreg. ATG)
pHTL-11		core(full-length)	MS
pHTL-12		core(Δ 8)	MS
pHTL-13	core(full-length)	S	

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PLASMID	PROMOTER		
	p7.5	p11	modified p7.5
pHTL-14	preS1-core(Δ 8)		MS
pHTL-15	core(full-length)		S
pHTL-17	core(full-length)		MS
pHTL-18	preS1-core(full-length)		MS
pHTL-23		preS1-core(Δ 8)	
pHTL-24		preS1-core(full-length)	
pHTL-25			core(full-length)
pHTL-26			core-preS1*
pHTL-27			core-preS2
pHTL-28			core-S*
pHTL-30	core(Δ 8)		MS (upreg. ATG)
pHTL-31	preS1-core(Δ 8)		MS (upreg. ATG)
pHTL-32	preS1-core(Δ 8)		
pHTL-33	core(full-length)		MS (upreg. ATG)
pHTL-34	core(full-length)		S
pHTL-35	core(full-length)		LS
pHTL-36	preS1-core(full-length)		MS (upreg. ATG)
pRO-10		S	
pRO-11	MS	S	
pRO-13B	LS		
pRO-16	core(Δ 8)	S	
pRO-16M	core(Δ 8)		
pRO-17	MS	core(Δ 8)	
pRO-18	LS	core(Δ 8)	
pRO-19		core(Δ 8)	

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PLASMID	PROMOTER		
	p7.5	p11	modified p7.5
pRO-19/24		core(full-length)	
pRO-21	MS	preS1-core(Δ 8)	
pRO-22	MS	core(full-length)	
pRO-23	MS	preS1-core(full-length)	

Other vectors which were constructed, and which have utility in generating the recombinant viruses of the invention upon further manipulation (with respect to the cloning vectors), or with a plasmid that provides T7 polymerase (with respect to HBV sequences operably linked to a T7 promoter) are also described *infra*.

6.1. SUBCLONING OF HBV GENES

The HBV genome, showing the core and surface antigen-encoding regions, is illustrated schematically in Figure 8. Using standard recombinant DNA techniques (see, for example, Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2nd ed., Cold Spring Harbor Press, New York), each of the four HBV genes were subcloned separately from the cloned HBV genome and placed in individual plasmids such that multiple restriction enzyme digestion sites surrounded each gene and provided for easy manipulation. A method used to make these subclones is described below. Unless otherwise mentioned, all DNA-modifying enzymes were obtained commercially from New England Biolabs (Beverly, MA) or BRL Life Technologies, Inc. (Gaithersburg, MD), and were used according to the manufacturer's instructions.

6.1.1. SURFACE ANTIGENS

The HBV genome (subtype adw) is contained in plasmid pAM6 (Moriarty et al., 1981, Proc. Natl. Acad. Sci. USA 78:2606-2610, available from the American Type Culture Collection (ATCC) Accession No. 45020, Fig. 9), a pBR322-based vector that is replicable in *E. coli*. Since the MS/LS open reading frames (ORFs) in pAM6 are interrupted by pBR322 DNA, these ORFs were resected using the 2883 bp cloning vector pT7T318 (Pharmacia cat. no. 27-3512; Fig. 10), which contains multiple restriction sites.

The 5' end of the open reading frame coding for the three surface antigens, which is bounded by BamHI and BglII restriction endonuclease sites in pAM6, a fragment of length 799 bp, was removed from pAM6 and inserted into BamHI-linearized pT7T318 to generate plasmid pRO-01 (Fig. 11). Briefly, pAM6 plasmid DNA was double digested with BamHI and BglII enzymes, and the fragments generated by the digestion were electrophoretically separated on an 0.8% agarose gel with appropriate size markers in 1X TBE (89.2 mM Tris pH 8.0, 89 mM boric acid, 2 mM EDTA), and the fragment corresponding to the 799 bp insert containing preS1 and part of preS2 was excised from the ethidium-bromide stained gel. This fragment was eluted from the gel by electrophoresis into a dialysis bag in 0.5X TBE and ligated, using T4 DNA ligase, to the pT7T318 DNA which had been linearized by BamHI digestion, similarly gel-purified, and treated with bacterial alkaline phosphatase (BAP) to prevent recircularization of the vector. A fraction of the ligation mix was transformed into *E. coli* (strain DH5 α F'I^Q, available from BRL Life Technologies, Inc., cat. no. 8288SA) which had previously been made competent to take up the DNA by standard techniques

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(Sambrook et al., *supra*). The transformed cells were plated on plates of LB agar plus 50 μ g/ml ampicillin to select for cells which had been transformed with the plasmid. Small 1 ml cultures of LB broth (10 g/l
5 bactotryptone, 5 g/l bacto-yeast extract, 10 g/l NaCl pH 7.5) plus 50 μ g/ml ampicillin were then grown. DNA was prepared from these cultures by a boiling lysis miniprep protocol (Sambrook et al., *supra*) followed by digestion and electrophoresis on an agarose gel to
10 screen for a colony containing an insert of the expected size and orientation. Specifically, the size and desired orientation of the insert was verified by digestion with PstI, which cuts in the polylinker of pT7T318 and within the insert, 5 bp from the 3' end of
15 the preS2 region. In the desired orientation, digestion of pRO-01 with PstI yields fragments of 812 bp and 2870 bp, consistent with the PstI site of the pT7T318 polylinker being at the N-terminus of the open reading frame. Large quantities of the desired
20 DNA and a glycerol stock of the plasmid-harboring *E. coli* were prepared by standard methods from a 250 ml LB broth plus ampicillin culture of the chosen colony.

The 3' end of the ORF coding for the three surface antigens was manipulated using similar
25 techniques to connect it to the 5' end of the ORF. Specifically, the 3'-end fragment with length 1372 bp was excised from pAM6 by BamHI digestion and purified from an agarose gel. This fragment was inserted into BamHI-linearized and bovine alkaline phosphatase
30 (BAP)-dephosphorylated pRO-01, a fragment of 3683 bp, to generate pRO-02 (Fig. 12), which contains an intact open reading frame capable of encoding LS, MS and S antigens. The correct orientation of the insert in pRO-02 was verified by double digestion with PstI and

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XbaI to yield a restriction pattern consistent with fragments of sizes 4018, 800, 224 and 12 bp.

In order to achieve a high level of expression of the genes encoding the LS, MS, and S antigens, each gene was engineered so as to be under the transcriptional control of a vaccinia or vaccinia-like promoter, i.e., a promoter which is recognized by vaccinia virus RNA polymerase. In nature, the 3' end of the vaccinia promoter is often very close to, in the case of early promoters, or superimposed on, in the case of late promoters, the translation initiation codon of the ORF (1990, Virology, Fields, B.N., ed., Raven Press, New York), so we deemed this proximity also desirable in recombinant constructs. With this goal in mind, the individual S, MS, or LS ORFs were subcloned back into pT7T318 to place restriction endonuclease sites close to the initiating ATG of each ORF. Using these sites, the vaccinia or vaccinia-like promoters were placed very close to the initiating ATG of each ORF.

The translational initiation codons of the MS and S ORFs are contained within a 321 bp HincII fragment of pRO-02. This HincII fragment was isolated from pRO-02 and cloned into HincII-linearized and BAP-treated pT7T318 to generate pRO-03 (Fig. 13). The correct orientation of the inserted fragment was verified by digestion of pRO-03 with BamHI to yield a restriction pattern consistent with fragments of 201 bp and 3003 bp, indicating that the insert had been made such that the BamHI site in the pT7T318 polylinker was located at the 3' end of the insert.

From pRO-03, the initiating ATG of the S ORF was subcloned so as to be in close proximity to useful restriction sites. Specifically, pRO-03 was digested with NlaIII, which digests the plasmid in many places

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(11 sites) including within the MS-encoding region one base pair upstream of the initiating ATG of the S ORF. NlaIII-digested pRO-03 was also digested with HincII, which cuts the plasmid at the 3' end of the S-fragment insert. The 67 bp ATG-containing fragment generated by this NlaIII/HincII digestion was then isolated from a 5.5% polyacrylamide gel run with appropriate size standards and then cloned into the vector backbone of pT7T318 which had been double digested with SphI and HincII, generating pRO-05 (Fig. 14), which contains the initiating ATG of the S ORF. The presence of the insert in pRO-05 was verified by double digestion with HindIII and EcoRI to yield a restriction pattern consistent with fragments of lengths 103 and 2871 bp. The orientation of the insert in pRO-05 was verified by restriction digestion to be such that the HincII site at the carboxyl-terminus of the inserted ORF is retained.

In a similar manner, the initiating ATG of MS was subcloned so as to be closely surrounded by restriction sites. Specifically, pRO-03 was digested with HaeIII, which cuts pRO-03 at 12 sites including one just two base pairs 5' of the initiating ATG of MS, together with HincII. The resulting 232 bp fragment containing the 5' end of the MS ORF was isolated and subcloned into the 2866 bp vector backbone of pT7T318 which had been double digested by SmaI and HincII, BAP-treated, and gel-purified, generating pRO-06 (Fig. 15). The size and orientation of the insert were verified by double digestion with HincII and EcoRI to yield a restriction pattern consistent with fragments of length 248 bp and 2850 bp.

The 3' end of the S antigen coding region was then added to the S ORF in pRO-05 by HincII and

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StuI double digestion of pRO-02 and isolation of the 750 bp fragment coding for this C-terminal region. This fragment was inserted into the 2918 bp HincII and SmaI double digested vector fragment of pRO-05 to
5 generate pT7T3/S (Fig. 16). Restriction analysis was used to confirm that the orientation of the insert in pT7T3/S was such that the HincII site within the S ORF had been recreated. pT7T3/S thus contains DNA
10 antigen, beginning with the initiating ATG.

In a similar manner, the 3' end of the S antigen was added to the MS ORF in pRO-06 by double digesting pRO-02 with HincII and SphI, isolating the fragment corresponding to the 1016 bp 3' end, and
15 inserting this fragment into the 3085 bp vector fragment of HincII and SphI double digested pRO-06, generating pT7T3/S2 (Fig. 17). Restriction analysis was used to verify that the insert's orientation in pT7T3/S2 was such that the HincII site within the S
20 region had been recreated. pT7T3/S2 created in this manner contains DNA encoding the entire open reading frame of the MS antigen, beginning with the initiating ATG of MS.

A plasmid construct containing the LS open
25 reading frame closely surrounded by restriction endonuclease sites was constructed using a similar procedure. The 509 bp HincII fragment of pAM6 containing the LS ATG was subcloned into HincII-linearized pT7T318, generating pLEH-01 (Fig.
30 18). pLEH-01 was then double digested with NlaIII, which cuts 10 times including at a site 1 base pair 5' of the initiating ATG of LS, and with HincII at a site approximately 230 base pairs 3' of the ATG. This fragment of 234 bp, containing the 5' end of the LS
35 ORF, was subcloned into the 2869 bp vector backbone of

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pt7T318 which had been double digested with SphI and HincII to give pLEH-02 (Fig. 19). Restriction analysis was used to confirm the size of the insert in pLEH-02 and that the insert was oriented so as to

5 recreate the HincII site. The 132 bp middle fragment of the LS ORF stretching from within preS1 to within preS2 was then subcloned from HincII/BamHI-cut pRO-02, into the 3091 bp vector backbone of pLEH-02 which had been double digested with HincII and BamHI, generating

10 pLEH-03 (Fig. 20). Restriction digestion was used to verify that the insert in pLEH-03 was oriented so as to restore both the HincII and BamHI sites, and that an insert of the expected size had been made.

Finally, the 938 bp portion of the LS ORF coding for

15 the C-terminus of LS was subcloned from pRO-02 which had been BamHI/StuI-digested, into the 3218 bp vector backbone of BamHI/SmaI-digested pLEH-03, generating pLEH-04 (Fig. 21). Restriction digests were used to confirm the size of the insert in pLEH-04, and that

20 the insert had been made so as to reconstruct the BamHI site within the preS2 region.

To verify the DNA sequences of the subcloned S, MS, and LS regions, the dideoxy method (e.g., Sequenase kit, United States Biochemical Corp.; Tabor

25 and Richardson, 1989, J. Biol. Chem. 214:6447-6458) was used to sequence double stranded DNA from pT7T3/S, pT7T3/S2, and pLEH-04 inwards from primers (M13 Single Strand Primer, Pharmacia LKB cat. no. 27-1534-03, and M13 Reverse Sequence Primer, Cat no. 27-1532-01)

30 complementary to both ends of the polylinker. In addition, a primer hybridizing just 3' of the ATG of the S ORF was used to facilitate sequencing of the 5' ends of the MS- and LS-encoding sequences. In order to sequence the interior of the S coding region, a 530

35 bp internal BalI/DraI fragment of the S region was

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subcloned into pT7T318 which had been linearized with HincII. Sequence data generated using this strategy was analyzed in comparison to the published sequence of one isolate of subtype adw DNA (Ono et al., 1983, Nucl. Acids Res. 11:1747-1757). When we performed these experiments, our sequence data showed three translatable open reading frames corresponding to DNA encoding LS, MS and S. The nucleotide and deduced amino acid sequences of the LS (SEQ ID NO: 5 and NO: 6), MS (SEQ ID NO: 7 and NO: 8), and S (SEQ ID NO: 9 and NO: 10) regions are shown in Figures 22, 23, and 24, respectively. Changes in nucleotide and amino acid sequence from the published sequence are noted in Table 4 and are believed to result from variability within the adw subtype.

TABLE 4

Comparison of Published HBV Surface ORFs (subtype adw)* and Surface ORFs in pLEH-04

Base of Change Relative to A of ATG	Region of Change	Published Triplet	Published Amino Acid	pLEH-04 Triplet	pLEH-04 Amino Acid
27	preS1	A A C	Asn	A A T	Asn
40	preS1	C T T	Leu	T T T	Phe
83, 84	preS1	A C A	Thr	A A C	Asn
166	preS1	C T C	Leu	T T C	Phe
187	preS1	A T T	Ile	G T T	Val
336	preS2	A A T	Asn	A A C	Asn
348	preS2	T T G	Leu	T T C	Phe
388	preS2	C T T	Leu	T T T	Arg
488	preS2	A T C	Ile	A A C	Asn
887	S	A A G	Lys	A T G	Met
954	S	T C C	Ser	T C T	Ser

Ono, T. et al., Nucleic Acids Research 11:1747-1757 (1983).

6.1.2. CORE ANTIGENS

Hepatitis B virus core antigen-encoding sequences were also subcloned and engineered so as to be transcriptionally controlled by a vaccinia or
5 vaccinia-like promoter. Like the surface antigen constructs, the hepatitis B core antigen constructs were designed so as to maintain a close proximity between the vaccinia promoter and the translational initiation codon of the core open reading frame. A
10 gene encoding a full-length core was used. In addition, a deleted version of the core gene, referred to as core Δ 8, in which 8 amino acids are deleted as set forth below starting 16 amino acids from the 3' end of the full-length core antigen, was used.

15 Core Δ 8:

pAM6 was digested with StyI at two sites, one 16 bp upstream of the initiating ATG of core and the second 5 bp downstream of the C-terminal end of the core antigen coding region, and the overhanging
20 single-stranded ends were blunted by treatment with Klenow fragment of DNA polymerase I by standard protocols. This 584 bp fragment was then gel-purified and subcloned into HincII-linearized pT7T318, generating a new plasmid, named pRO-09B (Fig. 25),
25 containing three BglII sites. The orientation of the insert in pRO-09B was determined to be such that the EcoRI site in the polylinker of pT7T318 is located at the C-terminus of the open reading frame; digestion with BglII and EcoRI yielded a restriction map
30 consistent with fragments of 24, 68, 420, and 2954 bp.

The 24 bp core Δ 8 deletion was generated using a partial BglII digest. By adjusting reaction conditions, it was possible to limit the action of BglII such that some of the product of the reaction
35 was cut only at one of the three BglII sites in core.

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This linearized plasmid, which consisted of a mixture of the pRO-09B plasmid which had been linearized at BglII site #1, BglII site #2, and BglII site #3, was then gel-purified. This linear product was then
5 digested to completion with SmaI at the 3' end of the polylinker, and the large 3390 bp and 3414 bp vector fragments corresponding to initial linearization at either BglII #2 or BglII #3 were gel-purified. The
10 158 bp BglII/HincII fragment of pAM6 containing the C-terminus of the core ORF was then subcloned into the purified vector mixture. The resultant minipreps were screened for the presence of a 420 bp band upon BglII digestion, indicative of insertion in the correct orientation in which the BglII site has been
15 recreated. The core regions of a number of candidate minipreps were sequenced to identify a clone in which BglII #2 was the site of digestion in the initial partial digest. The resulting plasmid, called pT7T3/C (Fig. 26), contained the expected 24 bp BglII-BglII
20 deletion from bases 508 to 531 of the core ORF, and also had an unexpected single base pair deletion of an adenine residue at base 237 of 555 total base pairs within the full-length core open reading frame in comparison with the published sequence (Ono et al.,
25 *supra*). Since this deletion would result in a frame-shift upon translation of the core RNA, a method of reinserting this base into the open reading frame was used, as described below. Besides our intentional 24 bp deletion and this unintentional deletion at base
30 237, we found 11 additional nucleotides which differed from the published wild-type core sequence, which are summarized in Table 5. Only one of these nucleotide changes results in a change in amino acid sequence.

TABLE 5

Comparison of Published HBV Core (subtype adw)*
and Core in pCODM/24

	Base of Change Relative to A of ATG	Published Triplet	Published Amino Acid	pCODM/24 Triplet	pCODM/24 Amino Acid
5	81	G T A	Val	G T C	Val
	82	C G A	Arg	A G A	Arg
	117	C G A	Arg	C G G	Arg
10	156	C A T	His	C A C	His
	159	A C T	Thr	A C C	Thr
	229, 231	C A A	Gln	G A G	Glu
	243	T C C	Ser	T C A	Ser
	246	A G A	Arg	A G G	Arg
	288	A A G	Lys	A A A	Lys
15	291	A T C	Ile	A T T	Ile
	360	G T C	Val	G T A	Val

* Ono, T. et al., Nucleic Acids Research 11:1747-1757 (1983).

20 To reinsert the missing adenine at base 237
of the core ORF, pT7T3/C was subjected to
oligonucleotide-directed site-specific mutagenesis on
double-stranded DNA by published techniques (see for
example Inouye, S. and Inouye, M.,

25 "Oligonucleotide-directed Site-specific Mutagenesis
Using Double-Stranded Plasmid DNA", in *Synthesis and
Applications of DNA and RNA*, ed. S. Narang, Academic
Press). (Polymerase chain reaction could also be used
to reinsert the missing nucleotide.) An.

30 oligonucleotide of sequence 5' GGA GGA TCC aGC ATC AAG
G 3' (SEQ ID NO:11) was used both to replace the
deleted base pair (lower case "a") and to generate for
cloning purposes, without changing the core protein's
amino acid sequence, a BamHI site (underlined) several
35 bases 5' of the missing base pair. Mutation using

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this procedure generated two types of DNA plasmids: wild-type and mutant containing the new BamHI site and the inserted adenine. The mutant DNA was then cloned selectively using this BamHI site, such that each of the two pieces of DNA on either side of the BamHI site were first cloned individually and then reunited. To do this, the transformed *E. coli* containing a mixture of mutated and non-mutated plasmids were inoculated into 250 ml LB broth with 50 µg/ml ampicillin, and a purified large-scale preparation of the DNA was made by standard techniques (Sambrook et al., *supra*). Separate aliquots of this DNA were then digested with either EcoRI/BamHI or HindIII/BamHI. Part of the EcoRI/BamHI-digested aliquot was subjected to electrophoresis on an agarose gel, and a 448 bp fragment was excised and purified. The same method was used to purify the 269 bp HindIII/BamHI fragment. Use of this method generated two fragments which were then used to make two plasmids: pT7T3/CHB (Fig. 27), in which the 269 bp 5' HindIII to BamHI region is cloned into the 2853 bp vector fragment of HindIII/BamHI digested pT7T318, and pT7T3/CRB (Fig. 28), in which the 448 bp 3' BamHI to EcoRI region is cloned into the 2862 bp vector fragment of BamHI/EcoRI-digested pT7T318. In both cases, the inserts were verified by restriction digestion to be oriented so as to recreate both restriction sites.

To reunite the core open reading frame, the 448 bp BamHI/EcoRI fragment of pT7T3/CRB containing the 3' end of the mutated open reading frame was then cloned into the 3101 bp fragment of BamHI/EcoRI-digested pT7T3/CHB so as to preserve both the BamHI and EcoRI sites, generating pT7T3/CODM (Fig. 29), which contains a complete coreΔ8 gene containing the desired single base pair insertion. The nucleotide

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sequence (SEQ ID NO:12) and deduced amino acid sequence (SEQ ID NO:13) of the core Δ 8 ORF in pT7T3/CODM are shown in Figure 30.

Full-length core:

- 5 In order to construct a full-length core gene, pT7T3/CRB was digested with BglII, which linearizes the plasmid, and ligated to a pair of oligonucleotides designed to hybridize to each other, add 24 bp of sequence, and leave overhanging
- 10 BglII-compatible ends. Oligonucleotides of sequence 5' GAT CCC AAT CGC GGC GTC GCA GAC 3' (SEQ ID NO:16) and 5' GAT CGT CTG CGA CGC GGC GAT TGG 3' (SEQ ID NO:17), were used for this purpose, and were designed to make changes in the nucleotide sequence at each end
- 15 of the insert so as to destroy both BglII sites but to still encode the correct amino acid sequence. By digesting the religated plasmid with BglII, selection was imposed for an insertion mutant, pCRB/24 (Fig. 31), which lacks BglII sites. pCRB/24 is similar to
- 20 pT7T3/CRB except that pCRB/24 encodes 8 additional amino acids of core antigen sequence and lacks any BglII sites. The correct orientation of the insert to recreate the authentic core amino acid sequence, and the fact that only a single insert had been made, was
- 25 confirmed by dideoxy sequencing of pCRB/24. To reconstruct the full-length core gene, pCRB/24 was digested with EcoRI and BamHI, and the 472 bp fragment containing the 3' end of the core gene was subcloned into the 3101 bp vector fragment of
- 30 EcoRI/BamHI-digested pT7T3/CHB to generate plasmid pCODM/24 (Fig. 32; Table 5, *supra*). The orientation of the insert in pCODM/24 was such that both the BamHI and EcoRI sites were recreated. pCODM/24 is identical to pT7T3/CODM except that pCODM/24 contains 24 bp
- 35 which are deleted in pT7T3/CODM. The nucleotide

sequence (SEQ ID NO:14) and deduced amino acid sequence (SEQ ID NO:15) of the core region in pCODM/24 are shown in Figure 33.

5 6.2. SINGLE EXPRESSION VECTORS FOR
 S, MS, LS AND CORE ANTIGENS

A variety of expression vectors for insertion into the vaccinia thymidine kinase gene was constructed in which p7.5 (Fig. 2), p11 (Fig. 4), or
10 the modified p7.5 promoter (Fig. 6) directed the expression of one of the cloned HBV genes. A number of constructs were made in which expression of a single HBV antigen was directed by the p7.5 promoter. To facilitate this, a unique XhoI restriction site was
15 created downstream of the p7.5 promoter in pGS53. This was done by linearizing pGS53 with BamHI, blunting the ends using Klenow treatment, setting up a ligation reaction in the presence of an excess of an XhoI linker of sequence 5' CCC TCG AGG G 3' (SEQ ID
20 NO:18) (New England Biolabs, cat. no. 1072), heating to denature, and religating. A fraction of this reaction was used to transform *E. coli* (DH5 α F'I^Q), and minipreps of colonies were screened for the presence of a new XhoI site. The plasmid thus
25 created, pGS53X (Fig. 34), contains two BamHI sites, one on each side of the XhoI site.

The 824 bp S fragment was then excised from pT7T3/S by digestion with HindIII and KpnI followed by treatment with T4 DNA polymerase in the presence of
30 deoxyribonucleotides. This treatment served to fill in overhanging 5' ends and remove overhanging 3' ends. The 1251 bp MS fragment was excised from pT7T3/S2 by digestion with KpnI and SphI followed again by T4 polymerase treatment. The 1325 bp LS fragment was
35 excised from pLEH-04 by digestion with HindIII and EcoRI followed by filling in the overhanging 5' ends

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with the Klenow fragment of DNA polymerase I. The ends of all three gel-purified fragments thus generated were made XhoI-compatible by addition of the XhoI linkers described above, which in this case had
5 been phosphorylated using T4 polynucleotide kinase and standard procedures, followed by digestion with XhoI. Each fragment was then subcloned into the 4704 bp XhoI-linearized and BAP-dephosphorylated pGS53X. The single antigen expression vectors thus created
10 contained the S gene, pGS53/S (Fig. 35), the MS gene, pGS53/S2 (Fig. 36), or the LS gene, pGS53/S1 (Fig. 37), each under the control of the p7.5 promoter. The orientation of each insert was determined using conventional restriction mapping to be such that each
15 open reading frame could be expressed from the p7.5 promoter. Specifically, the correct orientation of the insert was confirmed by HincII digestion to yield restriction maps consistent with fragments from pGS53/S of 352 and 5186 bp, from pGS53/S2 of 514 and
20 5447 bp, and from pGS53/S1 of 321, 520 and 5202 bp. The genes in these plasmids were engineered so that the 3' end of the p7.5 promoter in these vectors is within approximately 20 bp of the initiating ATG. In each of these constructs, the expression cassette
25 region is flanked by sequence from the vaccinia virus thymidine kinase gene. This thymidine kinase gene is contained in the HindIII-J fragment of the vaccinia genome.

A similar series of constructs for
30 expression of S, MS, and LS antigens individually directed by the modified p7.5 promoter and designed for insertion into the vaccinia TK gene was made as follows. The S region from pT7T3/S and the LS region from pLEH-04 were amplified by polymerase chain
35 reaction using techniques well known in the art

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(Erlich, H.A., ed., *PCR Technology, Principles and Applications for DNA Amplification*, M. Stockton Press, New York, 1989). One primer used was of sequence 5' CTC ACT CGA GGG AAT AAG CT 3' (SEQ ID NO:19), which
5 hybridizes from bases -23 to -4 relative to the initiating ATG in both plasmids. This primer contains a 2 bp change from the plasmid sequence, AA to CG at positions 7 and 8, which was designed to create an XhoI site (CTCGAG) upon amplification. Another primer
10 used, 5' TTG TTA GGC CTT AAA TGT AT 3' (SEQ ID NO:20), hybridizes at the carboxy-terminal end of the open reading frames in both of these plasmids (underlined nucleotides indicate position of termination codon TAA on the complementary strand). This primer contains a
15 2 bp change from the plasmid sequence, GT to CC at positions 9 and 10, designed to create a StuI site (AGGCCT) upon amplification. The fragments generated by PCR of pT7T3/S and pLEH-04 with these primers are expected to be of sizes 714 and 1203 base pairs,
20 respectively. These pieces were then digested with XhoI and StuI to remove the small fragments at either end, yielding fragments of size 699 and 1188 base pairs, respectively, which were purified from an agarose gel. These latter fragments were inserted
25 into the 4026 bp vector fragment of XhoI and StuI double digested pSC59 so as to reconstruct XhoI and StuI sites at each end of the insert. The S-containing construct named PHTL-8 (Fig. 38), and the LS containing construct, PHTL-9 (Fig. 39), each
30 consist of the modified p7.5 promoter situated so as to direct expression of the HBV antigen located downstream.

A construct designed to allow expression of the MS antigen from the modified p7.5 promoter was
35 made as follows. A 998 bp EcoRI-StuI fragment of

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pT7T3/S2 was gel-purified and inserted into the 4032 bp EcoRI-StuI digested vector fragment of pSC59 so as to reconstruct the EcoRI and StuI sites at either end of the insert. The resulting expression plasmid, PHTL-10 (Fig. 40), contains the MS ORF located downstream of the modified p7.5 promoter. PHTL-10 contains the sequence "CCCATG" surrounding the ATG of preS2. According to M. Kozak (1989, J. Cell Biol. 108:229-241), the DNA sequence leading to the strongest ribosome binding to a translation initiation codon is "ANNATG", where N is any nucleotide. In the absence of a strong consensus-like sequence surrounding the ATG of preS2, significant levels of expression of the S antigen from the MS-containing constructs may be observed by western blot. Polymerase chain reaction may be used to modify the surroundings of the preS2 ATG in PHTL-10 or other constructs to match this consensus sequence, as follows, with the goal of shifting expression from S to MS.

A fragment of PHTL-10 containing the initiating ATG of preS2 was amplified by PCR, and by the proper choice of primers the sequence upstream of the ATG was made to match the consensus sequence described by Kozak. One primer used was of the sequence 5' GAG CTC GGT ACC ACC ATG AAG TGG A 3' (SEQ ID NO:21), which hybridizes from bases -15 to +10 relative to the preS2 ATG and contains a KpnI site (GGTACC) as well as the desired C to A change at position 13. A second primer used in conjunction with this first primer is of sequence 5' GAG CAG GGG TCC TAG GAA TC 3' (SEQ ID NO:22). This second primer hybridizes to the opposite strand from the first primer, from bases +204 to +185 relative to the preS2 ATG in PHTL-10, and contains an AvrII site (CCTAGG).

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The product of a PCR reaction using these primers was digested with KpnI and AvrII, run on an agarose gel, and the 197 bp fragment containing the initiating ATG of MS was gel-purified. This fragment was cloned into
5 the 4833 bp gel-purified vector fragment of pHTL-10 generated by digestion with KpnI and AvrII so as to retain both restriction sites. Dideoxy sequencing was used to confirm that the expected changes had been made upstream of the initiating ATG of preS2 in the
10 new plasmid, pHTL-10M (Fig. 41), to match the consensus sequence. Western blotting was used to compare the relative expression levels of MS vs. S in pHTL-10 and pHTL-10M (see Section 8.2 *infra*). Analysis by Western blot probed with an anti-S
15 polyclonal antibody of proteins expressed transiently from pHTL-10 and pHTL-10M in vaccinia-infected cells showed that the amount of MS protein expressed from pHTL-10M was significantly increased and the amount of S protein significantly decreased relative to that
20 expressed from pHTL-10.

6.3. SINGLE EXPRESSION VECTORS FOR CORE-S-REGION FUSIONS

A series of expression constructs consisting
25 of fusions of the core antigen to the preS2 region or to part of the S or preS1 regions was also made. The fusion polypeptides were expressed from the modified p7.5 promoter (Fig. 6). The first step in generating core to S-region fusions was to subclone the full-
30 length core gene downstream of this promoter. This was done by digesting pCODM/24 with PstI, treating with mung bean nuclease (New England Biolabs) to remove single-stranded overhangs according to the manufacturer's directions, and then digesting with
35 EcoRI. The 727 bp fragment thus generated containing the wild-type core ORF was isolated and subcloned into

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the 4030 bp vector backbone of pSC59 which had been digested with XhoI, treated with mung bean nuclease, and then digested with EcoRI. Restriction digestion was used to verify that the insert was oriented so as to retain the EcoRI site at the C-terminal end of the core antigen. The resulting plasmid, pHTL-25 (Fig. 42), contains the full-length core antigen oriented so as to permit expression of the core from the modified p7.5 promoter. The expression cassette of promoter and antigen in pHTL-25 is flanked by pieces of the vaccinia TK gene to allow *in vivo* recombination of the plasmid into the vaccinia TK gene.

A vector was constructed to allow expression of a core-preS1 fusion polypeptide (called core-preS1*, because only a portion of preS1 is present). This core-preS1* fusion consists, starting at the amino terminus of the fusion protein, of amino acid residues 1 through 145 of core, a 3 amino acid spacer (ser-ala-cys), amino acids 1 through 56 of preS1, and a 4 amino acid tail (arg-pro-thr-ser; SEQ ID NO:56). To make this fusion vector, a piece of the preS1 region corresponding to the first 56 amino acids of preS1 was amplified by polymerase chain reaction from pLEH-04. We expected this region of preS1 to be immunogenic; data presented by Gassin et al. showed that the anti-preS1 immune responses of health workers vaccinated with a plasma-derived HBV vaccine were primarily against amino acid residues 12-27 and 32-53 (Gassin et al., 1990, Prevalence of preS1 peptides antibodies following HEVAC B vaccine, in *Progress in Hepatitis B Immunization*, Coursaget, P. and M.J. Tong, eds., John Libbey Eurotext, London). One primer used was of sequence 5' TCA CTA TCC GGA ATC AGC TT 3' (SEQ ID NO:23), which hybridizes from bases -22 to -3 relative to the ATG of preS1 and is designed

to introduce a BspEI site (TCCGGA) upon amplification and to destroy a potential termination codon (underlined C was changed from an A in pLEH-04). A second primer used was of sequence 5' GGT GAA TTC TGG CCC GAA TG 3' (SEQ ID NO:24), which hybridizes to the opposite strand from bases +171 to +152 of the preS1 region and is designed to create an EcoRI site (GAATTC) upon amplification. The product of the PCR reaction was double digested with BspEI and EcoRI, and the 178 bp product was gel-purified and cloned into the 4483 bp BspEI and EcoRI double digested vector fragment of PHTL-25 in an orientation which recreated both the EcoRI and BspEI sites at the ends of the insert. The resulting plasmid, PHTL-26 (Fig. 43), consists of the modified p7.5 promoter oriented so as to drive expression of the core-preS1* fusion. The nucleotide sequence (SEQ ID NO:25) and predicted amino acid sequence (SEQ ID NO:26) of the core-preS1* fusion made from PHTL-26 are shown in Figure 44.

Using a similar design to that of PHTL-26, a construct was made for expression of a fusion consisting, starting at the amino terminus of the fusion, of amino acid residues 1 through 144 of core, a one amino acid spacer (asp), residues 1 through 55 of preS2, residues 1 through 8 of S, and a 4 amino acid tail (arg-pro-thr-ser; SEQ ID NO:56). The preS2- and S-region insert in this construct was generated by polymerase chain reaction amplification of pLEH-04. One primer used was of sequence 5' CAT CCT CCG GAC ATG CAG TG 3' (SEQ ID NO:27), hybridizes from base +313 of the preS1 region to base +8 of preS2, and was designed to create a new BspEI site (TCCGGA) during amplification. A second primer which was used in conjunction with this first primer was of sequence 5' GTC CTA GGA ATT CTG ATG TG 3' (SEQ ID NO:28), which

hybridizes to the opposite strand from the first from bases +31 to +12 of the S region, and creates a new EcoRI site (GAATTC) during amplification. The product of PCR of pLEH-04 using these primers was digested
5 with EcoRI and BspEI, and the 190 bp fragment was gel-purified. This fragment was then cloned in a manner so as to regenerate EcoRI and BspEI sites at either end of the insert into the 4483 bp gel-purified vector fragment of pHTL-25 which had been double digested
10 with EcoRI and BspEI. The resulting plasmid, pHTL-27 (Fig. 45), is designed to allow expression of a core to preS2 fusion from the modified p7.5 promoter. The nucleotide sequence (SEQ ID NO:29) and predicted amino acid sequence (SEQ ID NO:30) of the core-preS2 fusion
15 made from pHTL-27 are shown in Figure 46.

A third construct of this type, consisting from the amino terminus of amino acid residues 1 through 144 of core, a one amino acid spacer (asp), residues 107 through 163 of the S antigen, and a
20 7 amino acid tail (asn-ser-gly-leu-leu-val-lys; SEQ ID NO:57) was made in a similar manner. This fusion polypeptide is referred to herein as core-S* because only a small portion of the S antigen, judged to be most important in terms of antigenicity, is
25 present. Hydrophilic stretches of the S antigen expected to contain antigenic determinants are located between residues 110 and 156 of S (Bhatnagar et al., 1982, Proc. Natl. Acad. Sci. USA 79:4400-4409). The nonapeptide sequence from 139 to 147 represents all or
30 an essential part of the a determinant of HBsAg, the major epitope in S against which humans make antibodies after exposure to any subtype of the hepatitis B virus (*id.*). A 197 bp piece of the S region containing these immunogenic regions was
35 generated by PCR amplification of pLEH-04 using

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primers 5' GTA TGT TTC CGG ATT GTC CT 3' (SEQ ID NO:31), which hybridizes from bases +304 to +323 of the S region and was designed to generate a BspEI site (TCCGGA) upon amplification, and 5' TGA GGC CGA ATT CCA TAG GT 3' (SEQ ID NO:32), which hybridizes to the opposite strand from bases +500 to +481 of S and was designed to create an EcoRI site (GAATTC) upon amplification. The product of PCR on pLEH-04 using these primers was double digested with EcoRI and BspEI, and the 172 bp product containing the S fragment was gel-purified. This fragment was then inserted, in a manner such that the restriction sites were regenerated at either end of the insert, into the 4483 bp vector fragment of pHTL-25 which had also been doubly digested with EcoRI and BspEI. The resulting plasmid was called pHTL-28 (Fig. 47). The nucleotide sequence (SEQ ID NO:33) and predicted amino acid sequence (SEQ ID NO:34) of the core-S* fusion made from pHTL-28 are shown in Figure 48.

20

6.4. DUAL EXPRESSION VECTORS

A number of constructs were made consisting of two promoters, divergently oriented and subcloned so as to be located within the vaccinia TK gene.

25 Various antigens were then subcloned downstream of one or both of the promoters, with the goal of allowing expression of two non-fused antigens from a single vaccinia recombinant containing the integrated plasmid. The first step in one scheme for making

30 these constructs was to delete the β -galactosidase gene from pSC10 by digesting the plasmid with BamHI and religating the larger fragment. The resulting plasmid, pSC10 Δ lacZ (Fig. 49), contains the 11 kD promoter located upstream of a unique BamHI site. At

35 this point, the p7.5 and p11 promoters were placed

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"back to back" to allow for future construction of a single expression vector capable of expressing two different antigens. To do this, the 117 bp XbaI-BamHI fragment of pSC10ΔlacZ was excised, blunted by Klenow treatment, and inserted into the 4690 bp fragment of pGS53 which had been linearized by HincII. The orientation of the insert in this new construct, pDPV (Fig. 50), was determined to be such that the two promoters are oriented back-to-back; double digestion with EcoRI and BamHI yielded a restriction map consistent with fragments of sizes 9, 35, 375 and 4392 bp. This process retains the XbaI site between the two promoters but destroys the BamHI site downstream of p11.

pDPV was modified to insert S downstream of the 11 kD promoter. This was done by cutting pDPV with XhoI and inserting the 834 bp S-containing XhoI fragment of pGS53/S into this 4811 bp linearized vector. Digestion of candidate miniprep DNAs with XbaI to yield restriction maps consistent with fragments of sizes 218, 1387, and 4040 bp was used to verify the correct orientation of the inserted S piece downstream of the p11 promoter in the resulting construct, pDPV-01 (Fig. 51). This construct contains an extra ATG 23 bp upstream of the S antigen initiating ATG which, if left in place, would interfere with proper expression of S from its own ATG. Oligonucleotide-directed mutagenesis was used to change this ATG to an ATA. One oligonucleotide used hybridizes to the strand containing the ATG from bases -12 to -30 relative to the initiating ATG of S, and has the sequence 5' CGA GGA ATT TAT TTA TAG C 3' (SEQ ID NO:35), where the underlined T indicates the base to be mutated. The sequence of the region upstream of

the S ATG in the resulting plasmid, pRO-10 (Fig. 52), was confirmed by dideoxy sequencing of the plasmid.

A vector, pRO-16 (Fig. 53), was constructed from pRO-10, allowing expression of the S antigen from the p11 promoter and the coreΔ8 antigen from the p7.5 promoter. This was done by cutting pT7T3/CODM with HindIII and EcoRI, filling in the overhanging 5' ends using the Klenow fragment of DNA polymerase I, and gel-purifying the 721 bp fragment containing the coreΔ8 antigen. This fragment was then subcloned into the 5645 bp vector fragment of SmaI-linearized pRO-10. The orientation of the insert in the resulting plasmid, pRO-16, was determined to be such that the two promoters were oriented back-to-back; BamHI digestion yielded a restriction map consistent with fragments of 275 and 6091 bp.

pRO-10 was modified to insert the MS antigen downstream of p7.5 as follows. The 1257 bp MS fragment was removed from pT7T3/S2 by double digestion with KpnI and HindIII, blunting the ends of the fragment with T4 DNA polymerase, and gel-purifying the 1.2 kb fragment. This piece was then inserted into SmaI-linearized, bacterial alkaline phosphatase (BAP)-treated pRO-10. The orientation of the insert in the resulting plasmid, pRO-11 (Fig. 54), was verified to be such that MS could be expressed from the p7.5 promoter; digestion with XbaI yielded fragments of sizes 218, 538, 1387 and 4759 bp. pRO-11 contains the S and MS ORFs downstream of p11 and p7.5, respectively.

The S fragment of pRO-11 was also replaced by coreΔ8. This was done by cutting pRO-11 with XhoI, blunting the ends of the pieces by Klenow treating, BAP-treating, and gel-purifying the vector fragment of 6072 bp. Into this blunt-ended vector was inserted

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the core Δ 8 fragment of pT7T3/CODM, generated by cutting pT7T3/CODM with HindIII and EcoRI, blunting the ends with Klenow, and gel-purifying the 721 bp core-containing region. Orientation of the insert in the resulting plasmid, pRO-17 (Fig. 55), was determined to be such that core Δ 8 could be expressed from the p11 promoter; digestion with BamHI yielded a restriction map consistent with fragments of sizes 49, 554 and 6090 bp. pRO-17 contains core Δ 8 downstream of the 11 kD promoter and MS downstream of the 7.5 kD promoter.

A plasmid analogous to pRO-17 but containing the full-length core gene instead of core Δ 8 was made in a manner identical to pRO-17, except that the 745 bp insert was cut from pCODM/24 instead of pT7T3/CODM. The same vector and restriction sites were used. The orientation of the insert in the resulting plasmid, pRO-22 (Fig. 56) was determined to be such that full-length core should be expressed from the 11 kD promoter; BamHI digestion yielded a restriction map consistent with fragments of sizes 49, 654 and 6114 bp.

A vector was also created containing only the divergently oriented p7.5 and p11 promoters by cutting pRO-10 with XhoI to excise the 834 bp S-containing fragment and religating the large 4811 bp vector fragment to delete the S region. The resulting plasmid, pRO-12 (Fig. 57), contains only the p7.5 and p11 promoters and no HBV antigens. This plasmid differs from pDPV in that it lacks the extra ATG downstream of the p11 promoter which was removed in the course of making pRO-10 from pDPV-01.

From pRO-12, a vector was created consisting of the LS antigen inserted downstream of p7.5. This construct was made by cutting the LS antigen from

pLEH-04 using a HindIII and EcoRI double digest, filling in the overhanging 5' ends by Klenow treatment, and gel-purifying the 1329 bp fragment. This LS fragment was then subcloned into the 4811 bp vector fragment of SmaI-digested, BAP-treated pRO-12. The orientation of the insert in the resulting plasmid, pRO-13B (Fig. 58), was determined to be such that LS should be expressible from p7.5; digestion with XbaI and PstI yielded a restriction map consistent with fragments of 125, 224, 641, 646, and 4504 bp. pRO-13B therefore consists of the p11 and p7.5 promoters oriented back-to-back with the LS open reading frame positioned downstream of p7.5.

The coreΔ8 antigen was inserted downstream of p11 in pRO-13B. This was done by digesting pT7T3/CODM with HindIII and EcoRI, filling in the overhanging 5' ends with the Klenow fragment, and gel-purifying the 721 bp coreΔ8-containing fragment. This fragment was then subcloned into the 6144 bp XhoI-linearized vector pRO-13B which had been Klenow- and then BAP-treated. The orientation of the insert in the resulting plasmid, pRO-18 (Fig. 59), was determined to be such that the coreΔ8 open reading frame should be expressed from the 11 kD promoter; digestion with BamHI yielded a restriction map consistent with fragments of sizes 376, 654 and 5835 bp.

A vector featuring coreΔ8 downstream of p11 was made by cutting pRO-17 with XbaI to remove the 1496 bp region containing the p11 promoter, core, and most of one-half of the vaccinia DNA, and cloning this piece into the 4040 bp XbaI-cut, BAP-treated vector fragment of pRO-12. Orientation of the insert in the resulting plasmid, pRO-19 (Fig. 60), was determined to be such that the two promoters, p7.5 alone and p11

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upstream of coreΔ8, were divergently oriented; digestion with BamHI yielded a restriction map consistent with fragments of sizes 654 and 4882 bp.

A plasmid analogous to pRO-19 containing the
5 p11-full-length core antigen cassette was made by cutting pCODM/24 with HindIII and EcoRI, blunting the ends by Klenow treatment, and gel-purifying the 745 bp fragment. This core-containing fragment was subcloned into the 4811 bp XhoI-linearized pRO-12 which had also
10 been made blunt-ended by Klenow. The resulting plasmid features full-length core downstream of p11. Orientation of the insert in the resulting plasmid, pRO-19/24 (Fig. 61), was determined to be such that the full-length core gene could be expressed from the
15 11 kD promoter; digestion with BamHI yielded a restriction map consistent with fragments of sizes 654 and 4906 bp.

To allow production of a series of constructs featuring the modified p7.5 promoter and
20 the p11 promoter back to back, another vector was made. pRO-19/24 was double digested with XbaI and EcoRI to excise the 893 bp fragment containing the p11-full-length core expression cassette. This fragment was gel-purified, the 5' overhanging ends
25 filled in by Klenow fragment of DNA polymerase I, and the piece subcloned into the 4042 bp vector fragment of pSC59 which had been digested with HindIII and treated with Klenow and BAP. To determine that the insertion had been made such that the two promoters,
30 p11 and the modified p7.5, were divergently oriented, the resulting plasmid, pHTL-5 (Fig. 62), was digested with PvuII and HindIII to yield a restriction pattern consistent with fragments of 1735 and 3200 bp. pHTL-5 contains the full-length core gene expressed from the

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p11 promoter, and the modified p7.5 promoter without any antigen cloned downstream.

From pHTL-5, plasmids expressing S or LS from the modified p7.5 promoter and full-length core
5 from the 11 kD promoter were made as follows. The S region from pT7T3/S and the LS region from pLEH-04 were removed by polymerase chain reaction using the same pair of primers. One primer used was of sequence 5' CTC ACT CGA GGG AAT AAG CT 3' (SEQ ID NO:36), and
10 was designed to hybridize from bases -23 to -4 relative to the initiating ATG in each plasmid and to generate an XhoI site (CTCGAG) upon amplification. A second primer used in conjunction with the first primer was of sequence 5' TTG TTA GGC CTT AAA TGT AT
15 3' (SEQ ID NO:37), and was designed to hybridize to the opposite strand from the first primer from bases +1179 to +1160 relative to the ATG of LS in pLEH-04 and from bases +690 to +671 relative to the ATG of S in pT7T3/S, and to generate a StuI site (AGGCCT) upon
20 amplification. The fragments generated by PCR using these primers on pT7T3/S and pLEH-04 were of sizes 714 and 1203 base pairs, respectively. These amplified fragments were digested with XhoI and StuI, removing a few base pairs at either end and yielding fragments of
25 size 699 and 1188 base pairs, respectively, which were purified from an agarose gel. These fragments were cloned so as to regenerate XhoI and StuI sites at either end of the insert, into the 4947 bp vector fragment of pHTL-5 which had been digested with XhoI
30 and StuI. The S- and LS-containing plasmids generated in this manner were called pHTL-6 (Fig. 63) and pHTL-7 (Fig. 64), respectively.

A similar construct consisting of MS expressed from the modified p7.5 promoter and the
35 full-length core antigen expressed from the 11 kD

promoter were made as follows. The 998 bp MS-containing fragment of EcoRI-StuI digested pT7T3/S2 was gel-purified and subcloned into the 4929 bp EcoRI-StuI vector fragment of pHTL-5. Restriction mapping was used to verify that the insertion had been made in an orientation so as to regenerate the EcoRI site at the 5' end encoding the amino terminus of the MS insert and the StuI site at the 3' end encoding the carboxyl terminus in the resulting plasmid, pHTL-11 (Fig. 65).

A plasmid for expressing MS from the modified p7.5 promoter and coreΔ8 from the p11 promoter was made from pHTL-11. To do this, a 849 bp AvrII-BspEI fragment of pHTL-11 containing the two promoters and the 5' end of each open reading frame was gel-purified and cloned into the 5742 bp AvrII-BspEI vector fragment of pRO-17 containing the 3' ends of MS and coreΔ8. The insert was made in such a way as to regenerate the AvrII and BspEI sites, and the resulting plasmid was called pHTL-12 (Fig. 66). In this plasmid, the coreΔ8 antigen has replaced the wild-type core antigen which was present in pHTL-11.

From pHTL-12 was made another construct, pRO-16M (Fig. 67), which consists of the coreΔ8 antigen cloned downstream of the p7.5 promoter. This construct was planned so as to delete an out-of-frame ATG which is present 31 bp upstream of the correct initiating ATG of coreΔ8 in pRO-16. pRO-16M was made by linearizing pRO-12 with BamHI, which cuts downstream of the p7.5 promoter, blunting the ends with Klenow treatment, and then treating with BAP. The 719 bp coreΔ8-containing insert was gel-purified from pHTL-12 which had been digested with PstI and then treated with mung bean nuclease. From the ligation of this fragment of pHTL-12 into the

linearized pRO-12 were chosen clones containing the coreΔ8 antigen situated downstream of p7.5. The presence and correct orientation of the insert in pRO-16M were determined by PstI/BspEI digestion, which
5 yielded a restriction pattern consistent with fragments of 850 and 4684 bp.

From pRO-16M was made an additional construct, pHTL-30 (Fig. 68), consisting of MS expressed from the modified p7.5 promoter and coreΔ8
10 expressed from the p7.5 promoter. The p7.5-coreΔ8 cassette was excised from pRO-16M by PCR. One primer used for this reaction was of sequence 5' GTG GGT AAG CTT CTC GAT GT 3' (SEQ ID NO:38) and is designed to hybridize from bases -230 to bases -211 relative to
15 the ATG of coreΔ8, upstream of the p7.5 promoter, and to create a HindIII site (AAGCTT) upon amplification. A second primer used in combination with the first primer was of sequence 5' AGT TTC CAA GCT TAT GAG 3' (SEQ ID NO:39), and was designed to hybridize to the
20 opposite strand from bases +563 to +546 and to generate a HindIII site upon amplification. The product of a PCR reaction using these two primers was digested with HindIII and the 774 bp fragment containing p7.5-coreΔ8 was gel-purified. This
25 fragment was inserted into pHTL-10M which had been linearized with HindIII just upstream of the modified p7.5 promoter and BAP treated. HindIII digestion was used to verify the presence of the insert in pHTL-30. Digestion with EcoRI/BspEI yielded a restriction map
30 consistent with fragments of 706 and 5098 bp, verifying that the two promoters were oriented back-to-back.

Using pHTL-5, a variant of pRO-16 consisting of S expressed from the p11 promoter and full-length
35 core, instead of coreΔ8, expressed from the p7.5

promoter was made. This was done by cutting pHTL-5 with BspEI and SacI to excise the 268 bp fragment coding for the carboxyl terminus of full-length core. This fragment was gel-purified and inserted into the 5 6123 bp vector fragment of pRO-16 which had been digested with BspEI and SacI and gel-purified. The orientation of the insert in the resulting plasmid, pHTL-13 (Fig. 69), was determined, based on the recreation of the BspEI and SacI sites, to be such 10 that the two promoters are divergently oriented.

From pHTL-13 was made a plasmid, pHTL-15 (Fig. 70), which contains the S antigen cloned downstream of the modified p7.5 promoter and full-length core cloned downstream of the p7.5 promoter. 15 This plasmid was made by digesting pHTL-13 with XbaI and SacI to excise the fragment containing the p7.5-full-length core cassette. This fragment was gel purified, treated with mung bean nuclease, and the 1008 bp resulting fragment inserted into the 4729 bp 20 vector fragment of pHTL-8 which had been linearized with BclI, Klenow filled, and BAP-treated. Presence of and correct orientation of the insert in pHTL-15 was verified by digestion with PstI to yield a restriction map consistent with pieces of 2223 and 25 3514 bp. This plasmid may be used for additional cloning; however, it is preferably not used for making recombinant vaccinia viruses because there is a segment of about 600 bp of vaccinia DNA between the two expression cassettes which may interfere with the 30 recombination of both cassettes into the vaccinia genome. However, by deletion of this sequence, a plasmid useful for making recombinant viruses can be made.

From pHTL-13 was made another plasmid, 35 pHTL-17 (Fig. 71), containing MS downstream of the

modified p7.5 promoter and full-length core downstream of the p7.5 promoter. This plasmid was made by digesting PHTL-13 with XbaI and SacI to excise the fragment containing the p7.5-full-length core cassette. This fragment was gel-purified, treated with mung bean nuclease, and the 1008 bp resulting fragment inserted into the 5034 bp vector fragment of PHTL-10 which had been linearized with BclI and Klenow filled. Presence of the insert in PHTL-17 was verified by digestion with PstI, which yielded a restriction map consistent with pieces of sizes 1000, 2223, and 2819 bp. Orientation of the insert was verified by this digest to be such that the two promoters are back-to-back. This plasmid may be used for additional cloning; however, it is preferably not used for making recombinant vaccinia viruses because there is a segment of about 600 bp of vaccinia DNA between the two expression cassettes which may interfere with the recombination of both cassettes into the vaccinia genome. However, by deletion of this sequence, a plasmid useful for making recombinant viruses can be made.

From PHTL-15 and PHTL-30 was made another plasmid, PHTL-33 (Fig. 72), consisting of full-length core cloned downstream of p7.5 and MS with the upregulated ATG cloned downstream of the modified p7.5 promoter. This plasmid was made by polymerase chain reaction amplification of the p7.5-full-length core cassette out of PHTL-15 using primers of the sequence 5' CTC GAT GTC GAC TAG CCA TA 3' (SEQ ID NO:58), which hybridizes to PHTL-15 from positions -237 to -218 relative to the ATG of core and the last four bases of which are part of an NdeI site (CATATG), and 5' AAG TTG TCG ACC TTA TGA GT 3' (SEQ ID NO:59), which hybridizes to the opposite strand from positions +587

to +568, downstream of the termination codon for full-length core, and which contains a Sall site (GTCGAC). The product of the PCR reaction was digested with Sall and NdeI and the 798 bp fragment containing the core expression cassette was isolated from an agarose gel and cloned into the 5046 bp gel purified vector fragment of PHTL-30 which had been digested with Sall and NdeI. Presence of the insert and situation of the two cassettes in a back-to-back orientation in PHTL-33 was determined by digestion with Sall and NdeI to yield a restriction map consistent with fragments of sizes 798 and 5046 bp.

From PHTL-33 was made an additional plasmid, PHTL-34 (Fig. 73), consisting of S expressed from the modified p7.5 promoter and full-length core expressed from the p7.5 promoter. This plasmid was made by digesting PHTL-8 with XhoI and ClaI and gel purifying the 767 bp fragment containing the S antigen. This fragment was cloned into the gel purified 4772 bp vector fragment of PHTL-33 which had also been digested with XhoI/ClaI. Presence and correct orientation of the insert in PHTL-34 were verified by digestion of the plasmid with XhoI/ClaI to yield a restriction map consistent with fragments of 767 and 4772 bp.

Also from PHTL-33 was made another plasmid, PHTL-35 (Fig. 74), consisting of LS expressed from the modified p7.5 promoter and full-length core expressed from the p7.5 promoter. This plasmid was made by gel purifying the 1256 bp XhoI/ClaI fragment of PHTL-9 containing the LS antigen and inserting it into the 4772 bp vector fragment of PHTL-33 which had also been digested with XhoI/ClaI. Presence and correct orientation of the insert in PHTL-35 were verified by digestion of the plasmid with XhoI and ClaI to yield a

various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the disclosures of which are incorporated by reference in their entireties.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Souw, Peter T.S.
O'Keefe, Rhonda W.
Lewis, Tatyana
Bernstine, Edward G.
- (ii) TITLE OF INVENTION: Hepatitis B Virus Vaccines
- (iii) NUMBER OF SEQUENCES: 59
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 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: On even date herewith
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
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 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Pro Arg Arg Arg Arg Ser Gln Ser
1 5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA

- 110 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATAAATAATA AATACAATAA TTAATTTCTC GTAAAAGTAG AAAATATATT CTAATTTATT 60
GCAC 64

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAGAAGCGA TGCTACGCTA GTCACAATCA CCACTTTCAT ATTTAGAATA TATGTATGTA 60
AAAATATAGT AGAATTTTCAT TTTGTTTTTT TCTATGCTAT AAAT 104

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAAATTGAA ATTTTATTTT TTTTTTTTGG AATATAAATA AG 42

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1170 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GGG ACG AAT CTT TCT GTT CCC AAT CCT CTG GGA TTC TTT CCC GAT 48
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

CAT CAG TTG GAC CCT GCA TTC GGA GCC AAC TCA AAC AAT CCA GAT TGG 96
His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

GAC TTC AAC CCC ATC AAG GAC CAC TGG CCA GCA GCC AAC CAG GTA GGA 144
Asp Phe Asn Pro Ile Lys Asp His Trp Pro Ala Ala Asn Gln Val Gly
35 40 45

- 111 -

GTG GGA GCA TTC GGG CCA GGG TTC ACC CCT CCA CAC GGC GGT GTT TTG Val Gly Ala Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Val Leu 50 55 60	192
GGG TGG AGC CCT CAG GCT CAG GGC ATA TTG ACC ACA GTG TCA ACA ATT Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Ser Thr Ile 65 70 75 80	240
CCT CCT CCT GCC TCC ACC AAT CGG CAG TCA GGA AGG CAG CCT ACT CCC Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro 85 90 95	288
ATC TCT CCA CCT CTA AGA GAC AGT CAT CCT CAG GCC ATG CAG TGG AAC Ile Ser Pro Pro Leu Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn 100 105 110	336
TCC ACT GCC TTC CAC CAA GCT CTG CAG GAT CCC AGA GTC AGG GGT CTG Ser Thr Ala Phe His Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu 115 120 125	384
TAT TTT CCT GCT GGT GGC TCC AGT TCA GGA ACA GTA AAC CCT GCT CCG Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Ala Pro 130 135 140	432
AAT ATT GCC TCT CAC ATC TCG TCA ATC TCC GCG AGG ACT GGG GAC CCT Asn Ile Ala Ser His Ile Ser Ser Ile Ser Ala Arg Thr Gly Asp Pro 145 150 155 160	480
GTG ACG AAC ATG GAG AAC ATC ACA TCA GGA TTC CTA GGA CCC CTG CTC Val Thr Asn Met Glu Asn Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu 165 170 175	528
GTG TTA CAG GCG GGG TTT TTC TTG TTG ACA AGA ATC CTC ACA ATA CCG Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro 180 185 190	576
CAG AGT CTA GAC TCG TGG TGG ACT TCT CTC AAT TTT CTA GGG GGA TCA Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ser 195 200 205	624
CCC GTG TGT CTT GGC CAA AAT TCG CAG TCC CCA ACC TCC AAT CAC TCA Pro Val Cys Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser 210 215 220	672
CCA ACC TCC TGT CCT CCA ATT TGT CCT GGT TAT CGC TGG ATG TGT CTG Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu 225 230 235 240	720
CGG CGT TTT ATC ATA TTC CTC TTC ATC CTG CTG CTA TGC CTC ATC TTC Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe 245 250 255	768
TTA TTG GTT CTT CTG GAT TAT CAA GGT ATG TTG CCC GTT TGT CCT CTA Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu 260 265 270	816
ATT CCA GGA TCA ACA ACA ACC AGT ACG GGA CCA TGC AAA ACC TGC ACG Ile Pro Gly Ser Thr Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr 275 280 285	864
ACT CCT GCT CAA GGC AAC TCT ATG TTT CCC TCA TGT TGC TGT ACA AAA Thr Pro Ala Gln Gly Asn Ser Met Phe Pro Ser Cys Cys Cys Thr Lys 290 295 300	912
CCT ACG GAT GGA AAT TGC ACC TGT ATT CCC ATC CCA TCG TCT TGG GCT Pro Thr Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala 305 310 315 320	960
TTC GCA AAA TAC CTA TGG GAG TGG GCC TCA GTC CGT TTC TCT TGG CTC Phe Ala Lys Tyr Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu	1008

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325	330	335	
AGT TTA CTA GTG CCA TTT GTT CAG TGG TTC GTA GGG CTT TCC CCC ACT			1056
Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr			
340	345	350	
GTT TGG CTT TCA GCT ATA TGG ATG ATG TGG TAT TGG GGG CCA AGT CTG			1104
Val Trp Leu Ser Ala Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu			
355	360	365	
TAC AGC ATC GTG AGT CCC TTT ATA CCG CTG TTA CCA ATT TTC TTT TGT			1152
Tyr Ser Ile Val Ser Pro Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys			
370	375	380	
CTC TGG GTA TAC ATT TAA			1170
Leu Trp Val Tyr Ile			
385	390		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1           5           10           15
His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
          20           25           30
Asp Phe Asn Pro Ile Lys Asp His Trp Pro Ala Ala Asn Gln Val Gly
          35           40           45
Val Gly Ala Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Val Leu
          50           55           60
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Ser Thr Ile
          65           70           75           80
Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro
          85           90           95
Ile Ser Pro Pro Leu Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn
          100          105          110
Ser Thr Ala Phe His Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu
          115          120          125
Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Ala Pro
          130          135          140
Asn Ile Ala Ser His Ile Ser Ser Ile Ser Ala Arg Thr Gly Asp Pro
          145          150          155          160
Val Thr Asn Met Glu Asn Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu
          165          170          175
Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
          180          185          190
Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ser
          195          200          205
Pro Val Cys Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser

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210	215	220
Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu 225 230 235 240		
Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe 245 250 255		
Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu 260 265 270		
Ile Pro Gly Ser Thr Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr 275 280 285		
Thr Pro Ala Gln Gly Asn Ser Met Phe Pro Ser Cys Cys Cys Thr Lys 290 295 300		
Pro Thr Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala 305 310 315 320		
Phe Ala Lys Tyr Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu 325 330 335		
Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr 340 345 350		
Val Trp Leu Ser Ala Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu 355 360 365		
Tyr Ser Ile Val Ser Pro Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys 370 375 380		
Leu Trp Val Tyr Ile 385		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 846 nucleotides
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG CAG TGG AAC TCC ACT GCC TTC CAC CAA GCT CTG CAG GAT CCC AGA Met Gln Trp Asn Ser Thr Ala Phe His Gln Ala Leu Gln Asp Pro Arg 1 5 10 15	48
GTC AGG GGT CTG TAT TTT CCT GCT GGT GGC TCC AGT TCA GGA ACA GTA Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val 20 25 30	96
AAC CCT GCT CCG AAT ATT GCC TCT CAC ATC TCG TCA ATC TCC GCG AGG Asn Pro Ala Pro Asn Ile Ala Ser His Ile Ser Ser Ile Ser Ala Arg 35 40 45	144
ACT GGG GAC CCT GTG ACG AAC ATG GAG AAC ATC ACA TCA GGA TTC CTA Thr Gly Asp Pro Val Thr Asn Met Glu Asn Ile Thr Ser Gly Phe Leu 50 55 60	192

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GGA CCC CTG CTC GTG TTA CAG GCG GGG TTT TTC TTG TTG ACA AGA ATC Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile 65 70 75 80	240
CTC ACA ATA CCG CAG AGT CTA GAC TCG TGG TGG ACT TCT CTC AAT TTT Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe 85 90 95	288
CTA GGG GGA TCA CCC GTG TGT CTT GGC CAA AAT TCG CAG TCC CCA ACC Leu Gly Gly Ser Pro Val Cys Leu Gly Gln Asn Ser Gln Ser Pro Thr 100 105 110	336
TCC AAT CAC TCA CCA ACC TCC TGT CCT CCA ATT TGT CCT GGT TAT CGC Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg 115 120 125	384
TGG ATG TGT CTG CGG CGT TTT ATC ATA TTC CTC TTC ATC CTG CTG CTA Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu 130 135 140	432
TGC CTC ATC TTC TTA TTG GTT CTT CTG GAT TAT CAA GGT ATG TTG CCC Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro 145 150 155 160	480
GTT TGT CCT CTA ATT CCA GGA TCA ACA ACA ACC AGT ACG GGA CCA TGC Val Cys Pro Leu Ile Pro Gly Ser Thr Thr Thr Ser Thr Gly Pro Cys 165 170 175	528
AAA ACC TGC ACG ACT CCT GCT CAA GGC AAC TCT ATG TTT CCC TCA TGT Lys Thr Cys Thr Thr Pro Ala Gln Gly Asn Ser Met Phe Pro Ser Cys 180 185 190	576
TGC TGT ACA AAA CCT ACG GAT GGA AAT TGC ACC TGT ATT CCC ATC CCA Cys Cys Thr Lys Pro Thr Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro 195 200 205	624
TCG TCT TGG GCT TTC GCA AAA TAC CTA TGG GAG TGG GCC TCA GTC CGT Ser Ser Trp Ala Phe Ala Lys Tyr Leu Trp Glu Trp Ala Ser Val Arg 210 215 220	672
TTC TCT TGG CTC AGT TTA CTA GTG CCA TTT GTT CAG TGG TTC GTA GGG Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly 225 230 235 240	720
CTT TCC CCC ACT GTT TGG CTT TCA GCT ATA TGG ATG ATG TGG TAT TGG Leu Ser Pro Thr Val Trp Leu Ser Ala Ile Trp Met Met Trp Tyr Trp 245 250 255	768
GGG CCA AGT CTG TAC AGC ATC GTG AGT CCC TTT ATA CCG CTG TTA CCA Gly Pro Ser Leu Tyr Ser Ile Val Ser Pro Phe Ile Pro Leu Leu Pro 260 265 270	816
ATT TTC TTT TGT CTC TGG GTA TAC ATT TAA Ile Phe Phe Cys Leu Trp Val Tyr Ile 275 280	846

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gln Trp Asn Ser Thr Ala Phe His Gln Ala Leu Gln Asp Pro Arg
1 5 10 15

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Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
 20 25 30
 Asn Pro Ala Pro Asn Ile Ala Ser His Ile Ser Ser Ile Ser Ala Arg
 35 40 45
 Thr Gly Asp Pro Val Thr Asn Met Glu Asn Ile Thr Ser Gly Phe Leu
 50 55 60
 Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile
 65 70 75 80
 Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe
 85 90 95
 Leu Gly Gly Ser Pro Val Cys Leu Gly Gln Asn Ser Gln Ser Pro Thr
 100 105 110
 Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg
 115 120 125
 Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu
 130 135 140
 Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro
 145 150 155 160
 Val Cys Pro Leu Ile Pro Gly Ser Thr Thr Thr Ser Thr Gly Pro Cys
 165 170 175
 Lys Thr Cys Thr Thr Pro Ala Gln Gly Asn Ser Met Phe Pro Ser Cys
 180 185 190
 Cys Cys Thr Lys Pro Thr Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro
 195 200 205
 Ser Ser Trp Ala Phe Ala Lys Tyr Leu Trp Glu Trp Ala Ser Val Arg
 210 215 220
 Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly
 225 230 235 240
 Leu Ser Pro Thr Val Trp Leu Ser Ala Ile Trp Met Met Trp Tyr Trp
 245 250 255
 Gly Pro Ser Leu Tyr Ser Ile Val Ser Pro Phe Ile Pro Leu Leu Pro
 260 265 270
 Ile Phe Phe Cys Leu Trp Val Tyr Ile
 275 280

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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ATG GAG AAC ATC ACA TCA GGA TTC CTA GGA CCC CTG CTC GTG TTA CAG Met Glu Asn Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln 1 5 10 15	48
GCG GGG TTT TTC TTG TTG ACA AGA ATC CTC ACA ATA CCG CAG AGT CTA Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu 20 25 30	96
GAC TCG TGG TGG ACT TCT CTC AAT TTT CTA GGG GGA TCA CCC GTG TGT Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ser Pro Val Cys 35 40 45	144
CTT GGC CAA AAT TCG CAG TCC CCA ACC TCC AAT CAC TCA CCA ACC TCC Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser 50 55 60	192
TGT CCT CCA ATT TGT CCT GGT TAT CGC TGG ATG TGT CTG CGG CGT TTT Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe 65 70 75 80	240
ATC ATA TTC CTC TTC ATC CTG CTG CTA TGC CTC ATC TTC TTA TTG GTT Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val 85 90 95	288
CTT CTG GAT TAT CAA GGT ATG TTG CCC GTT TGT CCT CTA ATT CCA GGA Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly 100 105 110	336
TCA ACA ACA ACC AGT ACG GGA CCA TGC AAA ACC TGC ACG ACT CCT GCT Ser Thr Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala 115 120 125	384
CAA GGC AAC TCT ATG TTT CCC TCA TGT TGC TGT ACA AAA CCT ACG GAT Gln Gly Asn Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp 130 135 140	432
GGA AAT TGC ACC TGT ATT CCC ATC CCA TCG TCT TGG GCT TTC GCA AAA Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Lys 145 150 155 160	480
TAC CTA TGG GAG TGG GCC TCA GTC CGT TTC TCT TGG CTC AGT TTA CTA Tyr Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu 165 170 175	528
GTG CCA TTT GTT CAG TGG TTC GTA GGG CTT TCC CCC ACT GTT TGG CTT Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu 180 185 190	576
TCA GCT ATA TGG ATG ATG TGG TAT TGG GGG CCA AGT CTG TAC AGC ATC Ser Ala Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile 195 200 205	624
GTG AGT CCC TTT ATA CCG CTG TTA CCA ATT TTC TTT TGT CTC TGG GTA Val Ser Pro Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val 210 215 220	672
TAC ATT TAA Tyr Ile 225	681

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Asn Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
 1 5 10 15
 Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
 20 25 30
 Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ser Pro Val Cys
 35 40 45
 Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
 50 55 60
 Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
 65 70 75 80
 Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
 85 90 95
 Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
 100 105 110
 Ser Thr Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala
 115 120 125
 Gln Gly Asn Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp
 130 135 140
 Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Lys
 145 150 155 160
 Tyr Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
 165 170 175
 Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
 180 185 190
 Ser Ala Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile
 195 200 205
 Val Ser Pro Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
 210 215 220
 Tyr Ile
 225

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 nucleotides
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAGGATCCA GCATCAAGG

19

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 534 nucleotides
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu 1 5 10 15	48
TCG TTT TTG CCT TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp 20 25 30	96
ACC GCC TCA GCT CTG TAT CGG GAA GCC TTA GAG TCT CCT GAG CAT TGC Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys 35 40 45	144
TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC TGC TGG GGG GAA Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu 50 55 60	192
TTG ATG ACT CTA GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala 65 70 75 80	240
TCA AGG GAT CTA GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys 85 90 95	288
ATT AGG CAA CTA TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 100 105 110	336
GAG ACT GTA CTT GAA TAT TTG GTA TCT TTC GGA GTG TGG ATT CGC ACT Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr 115 120 125	384
CCT CCA GCC TAT AGA CCA CCA AAT GCC CCT ATC TTA TCA ACA CTT CCG Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro 130 135 140	432
GAA ACT ACT GTT GTT AGA CGA CGG GAC CGA GGC AGG TCC CCT AGA AGA Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg 145 150 155 160	480
AGA ACT CCC TCG CCT CGC AGA CGC AGA TCT CAA TCT CGG GAA TCT CAA Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser Gln 165 170 175	528
TGT TAG Cys	534

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1           5           10           15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
          20           25           30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
          35           40           45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
          50           55           60
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
          65           70           75           80
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
          85           90           95
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
          100          105          110
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
          115          120          125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
          130          135          140
Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
          145          150          155          160
Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser Gln
          165          170          175
Cys

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC      48
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1           5           10           15
TCG TTT TTG CCT TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC      96
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
          20           25           30
ACC GCC TCA GCT CTG TAT CGG GAA GCC TTA GAG TCT CCT GAG CAT TGC      144
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
          35           40           45

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TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC TGC TGG GGG GAA Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu 50 55 60	192
TTG ATG ACT CTA GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala 65 70 75 80	240
TCA AGG GAT CTA GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys 85 90 95	288
ATT AGG CAA CTA TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 100 105 110	336
GAG ACT GTA CTT GAA TAT TTG GTA TCT TTC GGA GTG TGG ATT CGC ACT Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr 115 120 125	384
CCT CCA GCC TAT AGA CCA CCA AAT GCC CCT ATC TTA TCA ACA CTT CCG Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro 130 135 140	432
GAA ACT ACT GTT GTT AGA CGA CGG GAC CGA GGC AGG TCC CCT AGA AGA Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg 145 150 155 160	480
AGA ACT CCC TCG CCT CGC AGA CGC AGA TCC CAA TCG CCG CGT CGC AGA Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg 165 170 175	528
CGA TCT CAA TCT CGG GAA TCT CAA TGT TAG Arg Ser Gln Ser Arg Glu Ser Gln Cys 180 185	558

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu 1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp 20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys 35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu 50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala 65 70 75 80
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys 85 90 95
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 100 105 110
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr

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115	120	125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro		
130	135	140
Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg		
145	150	155
Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg		
165	170	175
Arg Ser Gln Ser Arg Glu Ser Gln Cys		
180	185	

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCCCAATC GCGGCGTCGC AGAC

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCGTCTGC GACGCGGCGA TTGG

24

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCTCGAGGG

10

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCACTCGAG GGAATAAGCT

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTGTTAGGCC TTAAATGTAT

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGCTCGGTA CCACCATGAA GTGGA

25

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAGCAGGGGT CCTAGGAATC

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCACTATCCG GAATCAGCTT

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGTGAATTCT GGCCCGAATG

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC	48
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu	
1 5 10 15	
TCG TTT TTG CCT TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC	96
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp	
20 25 30	
ACC GCC TCA GCT CTG TAT CGG GAA GCC TTA GAG TCT CCT GAG CAT TGC	144
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys	
35 40 45	
TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC TGC TGG GGG GAA	192
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu	
50 55 60	
TTG ATG ACT CTA GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA	240
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala	
65 70 75 80	
TCA AGG GAT CTA GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA	288
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys	
85 90 95	
ATT AGG CAA CTA TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA	336
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg	
100 105 110	
GAG ACT GTA CTT GAA TAT TTG GTA TCT TTC GGA GTG TGG ATT CGC ACT	384
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr	
115 120 125	
CCT CCA GCC TAT AGA CCA CCA AAT GCC CCT ATC TTA TCA ACA CTT CCG	432
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro	

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130	135	140	
GAA TCA GCT TGC ATG GGG ACG AAT CTT TCT GTT CCC AAT CCT CTG GGA			480
Glu Ser Ala Cys Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly			
145	150	155	160
TTC TTT CCC GAT CAT CAG TTG GAC CCT GCA TTC GGA GCC AAC TCA AAC			528
Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn			
165	170	175	
AAT CCA GAT TGG GAC TTC AAC CCC ATC AAG GAC CAC TGG CCA GCA GCC			576
Asn Pro Asp Trp Asp Phe Asn Pro Ile Lys Asp His Trp Pro Ala Ala			
180	185	190	
AAC CAG GTA GGA GTG GGA GCA TTC GGG CCA GAA TTC AGG CCT ACT AGT			624
Asn Gln Val Gly Val Gly Ala Phe Gly Pro Glu Phe Arg Pro Thr Ser			
195	200	205	
TAA			627

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Ser Ala Cys Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly
145 150 155 160

Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn
165 170 175

Asn Pro Asp Trp Asp Phe Asn Pro Ile Lys Asp His Trp Pro Ala Ala
180 185 190

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Asn Gln Val Gly Val Gly Ala Phe Gly Pro Glu Phe Arg Pro Thr Ser
 195 200 205

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 nucleotides
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATCCTCCGG ACATGCAGTG

20

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 nucleotides
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCCTAGGAA TTCTGATGTG

20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 639 nucleotides
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC	48
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu	
1 5 10 15	
TCG TTT TTG CCT TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC	96
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp	
20 25 30	
ACC GCC TCA GCT CTG TAT CGG GAA GCC TTA GAG TCT CCT GAG CAT TGC	144
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys	
35 40 45	
TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC TGC TGG GGG GAA	192

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Ser	Pro	His	His	Thr	Ala	Leu	Arg	Gln	Ala	Ile	Leu	Cys	Trp	Gly	Glu	
50						55					60					
TTG	ATG	ACT	CTA	GCT	ACC	TGG	GTG	GGT	AAT	AAT	TTG	GAG	GAT	CCA	GCA	240
Leu	Met	Thr	Leu	Ala	Thr	Trp	Val	Gly	Asn	Asn	Leu	Glu	Asp	Pro	Ala	
65					70				75						80	
TCA	AGG	GAT	CTA	GTA	GTC	AAT	TAT	GTT	AAT	ACT	AAC	ATG	GGT	TTA	AAA	288
Ser	Arg	Asp	Leu	Val	Val	Asn	Tyr	Val	Asn	Thr	Asn	Met	Gly	Leu	Lys	
				85				90						95		
ATT	AGG	CAA	CTA	TTG	TGG	TTT	CAT	ATA	TCT	TGC	CTT	ACT	TTT	GGA	AGA	336
Ile	Arg	Gln	Leu	Leu	Trp	Phe	His	Ile	Ser	Cys	Leu	Thr	Phe	Gly	Arg	
			100					105					110			
GAG	ACT	GTA	CTT	GAA	TAT	TTG	GTA	TCT	TTC	GGA	GTG	TGG	ATT	CGC	ACT	384
Glu	Thr	Val	Leu	Glu	Tyr	Leu	Val	Ser	Phe	Gly	Val	Trp	Ile	Arg	Thr	
		115					120					125				
CCT	CCA	GCC	TAT	AGA	CCA	CCA	AAT	GCC	CCT	ATC	TTA	TCA	ACA	CTT	CCG	432
Pro	Pro	Ala	Tyr	Arg	Pro	Pro	Asn	Ala	Pro	Ile	Leu	Ser	Thr	Leu	Pro	
		130				135					140					
GAC	ATG	CAG	TGG	AAC	TCC	ACT	GCC	TTC	CAC	CAA	GCT	CTG	CAG	GAT	CCC	480
Asp	Met	Gln	Trp	Asn	Ser	Thr	Ala	Phe	His	Gln	Ala	Leu	Gln	Asp	Pro	
145				150					155						160	
AGA	GTC	AGG	GGT	CTG	TAT	TTT	CCT	GCT	GGT	GGC	TCC	AGT	TCA	GGA	ACA	528
Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly	Gly	Ser	Ser	Ser	Gly	Thr	
				165					170					175		
GTA	AAC	CCT	GCT	CCG	AAT	ATT	GCC	TCT	CAC	ATC	TCG	TCA	ATC	TCC	GCG	576
Val	Asn	Pro	Ala	Pro	Asn	Ile	Ala	Ser	His	Ile	Ser	Ser	Ile	Ser	Ala	
			180					185					190			
AGG	ACT	GGG	GAC	CCT	GTG	ACG	AAC	ATG	GAG	AAC	ATC	ACA	TCA	GAA	TTC	624
Arg	Thr	Gly	Asp	Pro	Val	Thr	Asn	Met	Glu	Asn	Ile	Thr	Ser	Glu	Phe	
		195					200					205				
AGG	CCT	ACT	AGT	TAA												639
Arg	Pro	Thr	Ser													
		210														

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65 70 75 80

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[illegible]

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATGTTTCC GGATTGTCCT

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGAGGCCGAA TTCCATAGGT

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC	48
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu	
1 5 10 15	
TCG TTT TTG CCT TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC	96
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp	
20 25 30	
ACC GCC TCA GCT CTG TAT CGG GAA GCC TTA GAG TCT CCT GAG CAT TGC	144
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys	
35 40 45	
TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC TGC TGG GGG GAA	192
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu	
50 55 60	
TTG ATG ACT CTA GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA	240
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala	
65 70 75 80	
TCA AGG GAT CTA GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA	288
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys	
85 90 95	
ATT AGG CAA CTA TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA	336
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg	
100 105 110	
GAG ACT GTA CTT GAA TAT TTG GTA TCT TTC GGA GTG TGG ATT CGC ACT	384
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr	
115 120 125	
CCT CCA GCC TAT AGA CCA CCA AAT GCC CCT ATC TTA TCA ACA CTT CCG	432
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro	
130 135 140	
GAT TGT CCT CTA ATT CCA GGA TCA ACA ACA ACC AGT ACG GGA CCA TGC	480
Asp Cys Pro Leu Ile Pro Gly Ser Thr Thr Thr Ser Thr Gly Pro Cys	
145 150 155 160	
AAA ACC TGC ACG ACT CCT GCT CAA GGC AAC TCT ATG TTT CCC TCA TGT	528
Lys Thr Cys Thr Thr Pro Ala Gln Gly Asn Ser Met Phe Pro Ser Cys	
165 170 175	
TGC TGT ACA AAA CCT ACG GAT GGA AAT TGC ACC TGT ATT CCC ATC CCA	576
Cys Cys Thr Lys Pro Thr Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro	
180 185 190	
TCG TCT TGG GCT TTC GCA AAA TAC CTA TGG AAT TCA GGC CTA CTA GTT	624
Ser Ser Trp Ala Phe Ala Lys Tyr Leu Trp Asn Ser Gly Leu Leu Val	
195 200 205	
AAG TAA	
Lys	630

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1           5           10           15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
      20           25           30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
      35           40           45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
      50           55           60
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
      65           70           75           80
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
      85           90           95
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
      100           105           110
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
      115           120           125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
      130           135           140
Asp Cys Pro Leu Ile Pro Gly Ser Thr Thr Thr Ser Thr Gly Pro Cys
      145           150           155           160
Lys Thr Cys Thr Thr Pro Ala Gln Gly Asn Ser Met Phe Pro Ser Cys
      165           170           175
Cys Cys Thr Lys Pro Thr Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro
      180           185           190
Ser Ser Trp Ala Phe Ala Lys Tyr Leu Trp Asn Ser Gly Leu Leu Val
      195           200           205
Lys

```

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGAGGAATT ATTATAGC

19

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTCACTCGAG GGAATAAGCT

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTGTTAGGCC TTAAATGTAT

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTGGGTAAGC TTCTCGATGT

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGTTTCCAAG CTTATGAG

18

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

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GCGCCATGGA CATTGACCCT TATA

24

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCTGATCAC TAACATTGAG ATTCCCGA

28

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATTCTCGAGG GCATGGGGAC G

21

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACTCCATGGC CTGAGGATGA

20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 858 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATG GGG ACG AAT CTT TCT GTT CCC AAT CCT CTG GGA TTC TTT CCC GAT
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp

48

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1	5	10	15	
CAT CAG TTG GAC CCT GCA TTC GGA GCC AAC TCA AAC AAT CCA GAT TGG His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp 20 25 30				96
GAC TTC AAC CCC ATC AAG GAC CAC TGG CCA GCA GCC AAC CAG GTA GGA Asp Phe Asn Pro Ile Lys Asp His Trp Pro Ala Ala Asn Gln Val Gly 35 40 45				144
GTG GGA GCA TTC GGG CCA GGG TTC ACC CCT CCA CAC GGC GGT GTT TTG Val Gly Ala Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Val Leu 50 55 60				192
GGG TGG AGC CCT CAG GCT CAG GGC ATA TTG ACC ACA GTG TCA ACA ATT Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Ser Thr Ile 65 70 75 80				240
CCT CCT CCT GCC TCC ACC AAT CGG CAG TCA GGA AGG CAG CCT ACT CCC Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro 85 90 95				288
ATC TCT CCA CCT CTA AGA GAC AGT CAT CCT CAG GCC ATG GAC ATT GAC Ile Ser Pro Pro Leu Arg Asp Ser His Pro Gln Ala Met Asp Ile Asp 100 105 110				336
CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC TCG TTT TTG CCT Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro 115 120 125				384
TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC ACC GCC TCA GCT Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala 130 135 140				432
CTG TAT CGG GAA GCC TTA GAG TCT CCT GAG CAT TGC TCA CCT CAC CAC Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His 145 150 155 160				480
ACC GCA CTC AGG CAA GCC ATT CTC TGC TGG GGG GAA TTG ATG ACT CTA Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu 165 170 175				528
GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA TCA AGG GAT CTA Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu 180 185 190				576
GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA ATT AGG CAA CTA Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu 195 200 205				624
TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA GAG ACT GTA CTT Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu 210 215 220				672
GAA TAT TTG GTA TCT TTC GGA GTG TGG ATT CGC ACT CCT CCA GCC TAT Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr 225 230 235 240				720
AGA CCA CCA AAT GCC CCT ATC TTA TCA ACA CTT CCG GAA ACT ACT GTT Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val 245 250 255				768
GTT AGA CGA CGG GAC CGA GGC AGG TCC CCT AGA AGA AGA ACT CCC TCG Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser 260 265 270				816
CCT CGC AGA CGC AGA TCT CAA TCT CGG GAA TCT CAA TGT TAG Pro Arg Arg Arg Arg Ser Gln Ser Arg Glu Ser Gln Cys 275 280 285				858

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(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1           5           10           15
His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
          20           25           30
Asp Phe Asn Pro Ile Lys Asp His Trp Pro Ala Ala Asn Gln Val Gly
          35           40           45
Val Gly Ala Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Val Leu
          50           55           60
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Ser Thr Ile
          65           70           75           80
Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro
          85           90           95
Ile Ser Pro Pro Leu Arg Asp Ser His Pro Gln Ala Met Asp Ile Asp
          100          105          110
Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro
          115          120          125
Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala
          130          135          140
Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His
          145          150          155          160
Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu
          165          170          175
Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu
          180          185          190
Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu
          195          200          205
Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu
          210          215          220
Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr
          225          230          235          240
Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val
          245          250          255
Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser
          260          265          270
Pro Arg Arg Arg Ser Gln Ser Arg Glu Ser Gln Cys
          275          280          285

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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 nucleotides

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCGCCATGGA CATTGACCCT TATA

24

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 nucleotides
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGTGAAGCTT CCCACCTT

18

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 882 nucleotides
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATG GGG ACG AAT CTT TCT GTT CCC AAT CCT CTG GGA TTC TTT CCC GAT	48
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp	
1 5 10 15	
CAT CAG TTG GAC CCT GCA TTC GGA GCC AAC TCA AAC AAT CCA GAT TGG	96
His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp	
20 25 30	
GAC TTC AAC CCC ATC AAG GAC CAC TGG CCA GCA GCC AAC CAG GTA GGA	144
Asp Phe Asn Pro Ile Lys Asp His Trp Pro Ala Ala Asn Gln Val Gly	
35 40 45	
GTG GGA GCA TTC GGG CCA GGG TTC ACC CCT CCA CAC GGC GGT GTT TTG	192
Val Gly Ala Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Val Leu	
50 55 60	
GGG TGG AGC CCT CAG GCT CAG GGC ATA TTG ACC ACA GTG TCA ACA ATT	240
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Ser Thr Ile	
65 70 75 80	
CCT CCT CCT GCC TCC ACC AAT CGG CAG TCA GGA AGG CAG CCT ACT CCC	288
Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro	
85 90 95	

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ATC TCT CCA CCT CTA AGA GAC AGT CAT CCT CAG GCC ATG GAC ATT GAC Ile Ser Pro Pro Leu Arg Asp Ser His Pro Gln Ala Met Asp Ile Asp 100 105 110	336
CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC TCG TTT TTG CCT Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro 115 120 125	384
TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC ACC GCC TCA GCT Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala 130 135 140	432
CTG TAT CGG GAA GCC TTA GAG TCT CCT GAG CAT TGC TCA CCT CAC CAC Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His 145 150 155 160	480
ACC GCA CTC AGG CAA GCC ATT CTC TGC TGG GGG GAA TTG ATG ACT CTA Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu 165 170 175	528
GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA TCA AGG GAT CTA Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu 180 185 190	576
GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA ATT AGG CAA CTA Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu 195 200 205	624
TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA GAG ACT GTA CTT Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu 210 215 220	672
GAA TAT TTG GTA TCT TTC GGA GTG TGG ATT CGC ACT CCT CCA GCC TAT Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr 225 230 235 240	720
AGA CCA CCA AAT GCC CCT ATC TTA TCA ACA CTT CCG GAA ACT ACT GTT Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val 245 250 255	768
GTT AGA CGA CGG GAC CGA GGC AGG TCC CCT AGA AGA AGA ACT CCC TCG Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser 260 265 270	816
CCT CGC AGA CGC AGA TCC CAA TCG CCG CGT CGC AGA CGA TCT CAA TCT Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser 275 280 285	864
CGG GAA TCT CAA TGT TAG Arg Glu Ser Gln Cys 290	882

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

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Asp Phe Asn Pro Ile Lys Asp His Trp Pro Ala Ala Asn Gln Val Gly
 35 40 45
 Val Gly Ala Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Val Leu
 50 55 60
 Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Ser Thr Ile
 65 70 75 80
 Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro
 85 90 95
 Ile Ser Pro Pro Leu Arg Asp Ser His Pro Gln Ala Met Asp Ile Asp
 100 105 110
 Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro
 115 120 125
 Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala
 130 135 140
 Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His
 145 150 155 160
 Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu
 165 170 175
 Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu
 180 185 190
 Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu
 195 200 205
 Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu
 210 215 220
 Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr
 225 230 235 240
 Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val
 245 250 255
 Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser
 260 265 270
 Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser
 275 280 285
 Arg Glu Ser Gln Cys
 290

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTTGGTAGAA TTCCAATTAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- 137 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AAGAATGATC GATACAGTTT

20

- (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTACCCCGAA TTCATACTTA

20

- (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AATAATATAT CGATAATTGT

20

- (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTGGAATTC CGCTACTGAT

20

- (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TAACCAAGTA TCGATATAAT

20

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Arg Pro Thr Ser
1

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Asn Ser Gly Leu Leu Val Lys
1 5

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTCGATGTCG ACTAGCCATA

20

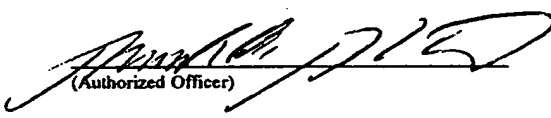
(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AAGTTGTCGA CCTTATGAGT

MICROORGANISMS	
Optional Sheet in connection with the microorganism referred to on page 107, lines 20-35 of the description	
A. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, MD 20852 US	
Date of deposit November 12, 1992 Accession Number 69124	
B. ADDITIONAL INDICATIONS (leave blank if not applicable). This information is continued on a separate attached sheet	
C. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not all designated States)	
D. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (Specify the general nature of the indications e.g., "Accession Number of Deposit")	
E. <input type="checkbox"/> This sheet was received with the International application when filed (to be checked by the receiving Office)	
 (Authorized Officer)	
<input type="checkbox"/> The date of receipt (from the applicant) by the International Bureau	
was _____ (Authorized Officer)	

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WHAT IS CLAIMED IS:

1. A recombinant replicable vaccinia virus, the genome of which comprises:

- 5 (a) a first nucleotide sequence encoding at least one epitope of a hepatitis B virus surface antigen;
- (b) a first promoter sequence operably linked to said first nucleotide sequence;
- 10 (c) a second nucleotide sequence encoding at least one epitope of a hepatitis B virus core antigen; and
- (d) a second promoter sequence operably linked to said second nucleotide sequence;
- 15

whereby the first and second nucleotide sequences are expressed by the virus in a suitable host.

- 20 2. The virus of claim 1 in which the first nucleotide sequence encodes an amino acid sequence comprising a protein selected from the group consisting of a hepatitis B virus S, MS, LS, preS2, preS1, derivatives of any of the foregoing displaying the antigenicity of any of the foregoing, and fusion
- 25 proteins consisting of combinations of S, MS, LS, preS2, preS1, and derivatives of any of the foregoing displaying the antigenicity of any of the foregoing; and the second nucleotide sequence encodes an amino acid sequence comprising a protein selected from the
- 30 group consisting of core antigen, e antigen, and derivatives thereof displaying the antigenicity of core antigen or e antigen.

35

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3. The virus of claim 1 which is infectious in the host without causing significant disease.

5 4. A recombinant replicable vaccinia virus, the genome of which comprises:

- 10 (a) a first nucleotide sequence encoding hepatitis B virus LS, MS, S, or a derivative of any of the foregoing displaying the antigenicity of any of the foregoing;
- (b) a first promoter sequence operably linked to said first nucleotide sequence;
- 15 (c) a second nucleotide sequence encoding a fusion protein comprising a first protein sequence containing at least one hepatitis B virus surface antigen epitope fused via a peptide bond to a
20 second protein sequence containing at least one hepatitis B virus core antigen epitope; and
- (d) a second promoter sequence operably linked to said second nucleotide
25 sequence;

whereby the first and second nucleotide sequences are expressed by the virus in a suitable host.

5. The virus of claim 4 in which the
30 fusion protein is selected from the group consisting of the following hepatitis B virus sequences: a preS1 region fused to a core antigen, a preS1 region fused to a core antigen derivative, a core antigen fused to S, a core antigen fused to a preS2 region, a core
35 antigen derivative fused to S, a core antigen

derivative fused to a preS2 region, a core antigen fused to a preS1 region, a core antigen derivative fused to a preS1 region, and a core antigen fused to a preS1 region derivative; in which the core antigen derivative displays the antigenicity of the hepatitis B virus core antigen, and the preS1 region derivative displays the antigenicity of the hepatitis B virus preS1 region.

6. The virus of claim 4 in which the fusion protein is selected from the group consisting of a core-preS1 fragment fusion protein having the amino acid sequence shown in Figure 44 (SEQ ID NO:26), a core-preS2 fusion protein having the amino acid sequence shown in Figure 46 (SEQ ID NO:30), a preS1-core Δ 8 fusion protein having the amino acid sequence shown in Figure 76 (SEQ ID NO:45), and a preS1-core fusion protein having the amino acid sequence shown in Figure 78 (SEQ ID NO:49).

7. The virus of claim 6 in which the first nucleotide sequence comprises the sequence encoding MS as shown in Figure 23 (SEQ ID NO:7).

8. The virus of claim 6 in which the first nucleotide sequence encodes said derivative, said derivative being a fusion protein comprising a third protein sequence containing at least one hepatitis B virus surface antigen epitope, which third protein sequence is fused via a peptide bond to a fourth protein sequence containing at least one hepatitis B virus core antigen epitope; with the proviso that the first nucleotide sequence and the second nucleotide sequence have sequences that do not overlap by more than 20 nucleotides.

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9. A recombinant replicable vaccinia virus, the genome of which comprises:

- (a) a first nucleotide sequence encoding a hepatitis B virus MS antigen;
- 5 (b) a first promoter sequence operably linked to said first nucleotide sequence;
- (c) a second nucleotide sequence encoding a fusion protein comprising a hepatitis B virus core antigen or a derivative thereof displaying core antigenicity, fused at its carboxy terminus via a peptide bond to the amino terminus of a hepatitis B virus preS1 region; and
- 10 (d) a second promoter sequence operably linked to said second nucleotide sequence;
- 15

whereby the first and second nucleotide sequences are expressed by the virus in a suitable host.

20

10. A recombinant replicable vaccinia virus, the genome of which comprises:

- (a) a first nucleotide sequence encoding a hepatitis B virus MS antigen;
- 25 (b) a first promoter sequence operably linked to said first nucleotide sequence;
- (c) a second nucleotide sequence encoding a fusion protein comprising a hepatitis B virus preS1 region fused at its carboxy terminus via a peptide bond to the amino terminus of a hepatitis B virus core antigen or a derivative thereof displaying core antigenicity; and
- 30

35

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(d) a second promoter sequence operably linked to said second nucleotide sequence;

whereby the first and second nucleotide sequences are
5 expressed by the virus in a suitable host.

11. The virus of claim 9 in which the core antigen or derivative thereof is a core antigen derivative having the amino acid sequence shown in
10 Figure 33 (SEQ ID NO:15) or in Figure 30 (SEQ ID NO:13).

12. The virus of claim 10 in which the core antigen or derivative thereof is a core antigen
15 derivative having the amino acid sequence shown in Figure 33 (SEQ ID NO:15) or in Figure 30 (SEQ ID NO:13).

13. The virus of claim 12 in which the
20 first promoter is modified p7.5, and the second promoter is p7.5.

14. The virus of claim 12 in which the first promoter is p7.5, and the second promoter is
25 p11.

15. A recombinant replicable vaccinia virus, the genome of which comprises:

(a) a first nucleotide sequence encoding a
30 first fusion protein comprising a first hepatitis B virus core antigen derivative displaying core antigenicity fused at its carboxy terminus via a peptide bond to the amino terminus of a
35 hepatitis B virus preS2 region;

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- (b) a first promoter sequence operably linked to said first nucleotide sequence;
- (c) a second nucleotide sequence encoding a second fusion protein comprising a hepatitis B virus preS1 region fused at its carboxy terminus via a peptide bond to the amino terminus of a second hepatitis B virus core antigen derivative displaying core antigenicity; and
- (d) a second promoter sequence operably linked to said second nucleotide sequence;
- with the proviso that the first and second nucleotide sequences have sequences that do not overlap by more than 20 nucleotides; whereby the first and second nucleotide sequences are expressed by the virus in a suitable host.

20

16. The virus of claim 15 in which the core antigen or derivative thereof is a core antigen derivative having the amino acid sequence shown in Figure 33 (SEQ ID NO:15) or in Figure 30 (SEQ ID NO:13).

25

17. The virus of claim 16 in which the first promoter is modified p7.5, and the second promoter is p7.5.

30

18. A recombinant replicable vaccinia virus, the genome of which comprises a nucleotide sequence encoding a hepatitis B virus core antigen derivative having the amino acid sequence shown in Figure 30 (SEQ ID NO:13); and a promoter sequence

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operably linked to said nucleotide sequence, whereby the nucleotide sequence is expressed by the virus in a suitable host.

5 19. A recombinant replicable vaccinia virus, the genome of which comprises a nucleotide sequence encoding a fusion protein, which protein comprises a first protein sequence containing at least one hepatitis B virus core antigen epitope, wherein
10 said first protein sequence is fused at its carboxy terminus via a peptide bond to a second protein sequence containing at least one hepatitis B virus surface antigen epitope; and a promoter sequence operably linked to said nucleotide sequence, whereby
15 the nucleotide sequence is expressed by the virus in a suitable host.

 20. A recombinant replicable vaccinia virus, the genome of which comprises a nucleotide
20 sequence encoding a fusion protein, which protein comprises a first protein sequence containing at least one hepatitis B virus surface antigen epitope, wherein said first protein sequence is fused at its carboxy terminus via a peptide bond to a second protein
25 sequence containing at least one hepatitis B virus core antigen epitope; and a promoter sequence operably linked to said nucleotide sequence, whereby the nucleotide sequence is expressed by the virus in a suitable host.

30

 21. The virus of claim 19 in which the fusion protein is selected from the group consisting of the following hepatitis B virus sequences: a core antigen or core antigen derivative fused to a preS1
35 region or preS1 derivative, core antigen or core

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antigen derivative fused to a preS2 region or preS2 derivative, or a core antigen or core antigen derivative fused to an S protein; in which the core antigen derivative displays the antigenicity of the
5 core antigen, the preS1 derivative displays the antigenicity of the preS1 region, the preS2 derivative displays the antigenicity of the preS2 region, and the S derivative displays the antigenicity of the S protein.

10

22. The virus of claim 1 in which the first and second nucleotide sequences are situated internally with respect to vaccinia virus thymidine kinase gene sequences, and the virus does not express
15 a functional thymidine kinase.

23. The virus of claim 4 in which the first and second nucleotide sequences are situated internally with respect to vaccinia virus thymidine
20 kinase gene sequences, and the virus does not express a functional thymidine kinase.

24. The virus of claim 9 in which the first and second nucleotide sequences are situated
25 internally with respect to vaccinia virus thymidine kinase gene sequences, and the virus does not express a functional thymidine kinase.

25. The virus of claim 10 in which the
30 first and second nucleotide sequences are situated internally with respect to vaccinia virus thymidine kinase gene sequences, and the virus does not express a functional thymidine kinase.

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26. The virus of claim 19 in which the nucleotide sequence is situated internally with respect to vaccinia virus thymidine kinase gene sequences, and the virus does not express a functional thymidine kinase.

27. Plasmid pHTL-31, as deposited with the ATCC and assigned accession number 69124.

28. A recombinant replicable vaccinia virus, the genome of which comprises:

- (a) a first nucleotide sequence that comprises the p7.5 promoter operably linked to a first coding sequence encoding a fusion protein consisting of a hepatitis B virus preS1 region fused to a hepatitis B virus core antigen derivative, as contained in plasmid pHTL-31; and
- (b) a second nucleotide sequence that comprises (i) the modified p7.5 promoter operably linked to a second coding sequence encoding a hepatitis B virus MS antigen, and (ii) a sequence upstream of the initiator ATG of the MS antigen that is associated with strong ribosome binding, as contained in plasmid pHTL-31;

wherein plasmid pHTL-31 is as deposited with the ATCC and assigned accession no. 69124.

29. The virus of claim 1 which further comprises a sequence upstream of the initiator ATG in the first nucleotide sequence, that matches a

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consensus sequence associated with strong ribosome binding.

30. The virus of claim 9 which further
5 comprises a sequence upstream of the initiator ATG for the MS antigen in the first nucleotide sequence, that matches a consensus sequence associated with strong ribosome binding.

10 31. The virus of claim 10 which further comprises a sequence upstream of the initiator ATG for the MS antigen in the first nucleotide sequence, that matches a consensus sequence associated with strong ribosome binding.

15 32. A vaccine formulation comprising the recombinant vaccinia virus of claim 1; and a pharmaceutically acceptable carrier.

20 33. A vaccine formulation comprising the recombinant vaccinia virus of claim 4; and a pharmaceutically acceptable carrier.

25 34. A vaccine formulation comprising the recombinant vaccinia virus of claim 9; and a pharmaceutically acceptable carrier.

30 35. A vaccine formulation comprising the recombinant vaccinia virus of claim 10; and a pharmaceutically acceptable carrier.

35 36. A vaccine formulation comprising the recombinant vaccinia virus of claim 15; and a pharmaceutically acceptable carrier.

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37. A vaccine formulation comprising a first recombinant virus of claim 1; a second recombinant virus of claim 1; and a pharmaceutically acceptable carrier; in which the first and second
5 recombinant viruses encode different hepatitis B virus amino acid sequences.

38. A vaccine formulation comprising a first recombinant virus of claim 4; a second
10 recombinant virus of claim 4; and a pharmaceutically acceptable carrier; in which the first and second recombinant viruses encode different hepatitis B virus amino acid sequences.

15 39. A vaccine formulation comprising a first recombinant virus of claim 19; a second recombinant virus of claim 19; and a pharmaceutically acceptable carrier; in which the first and second recombinant viruses express different fusion proteins.
20

40. A vaccine formulation comprising:
(a) a first recombinant replicable vaccinia virus, the genome of which comprises
(i) a first nucleotide sequence
25 encoding a first fusion protein, said first fusion protein comprising a hepatitis B virus core antigen or derivative thereof displaying core antigenicity, fused at its carboxy
30 terminus via a peptide bind to a hepatitis B virus preS1 region or derivative thereof displaying preS1 antigenicity, and (ii) a first promoter sequence operably linked to said first
35 nucleotide sequence, whereby the first

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- nucleotide sequence is expressed by
said first virus in a suitable host;
- (b) a second recombinant replicable
vaccinia virus, the genome of which
comprises (i) a second nucleotide
sequence encoding a second fusion
protein, said second fusion protein
comprising a hepatitis B virus core
antigen or derivative thereof
displaying core antigenicity, fused at
its carboxy terminus via a peptide bond
to a hepatitis B virus preS2 region or
derivative thereof displaying preS2
antigenicity, and (ii) a second
promoter sequence operably linked to
said second nucleotide sequence,
whereby the second nucleotide sequence
is expressed by said second virus in a
suitable host;
- (c) a third recombinant replicable vaccinia
virus, the genome of which comprises
(i) a third nucleotide sequence
encoding a hepatitis B virus S protein
or a derivative thereof displaying S
antigenicity, and (ii) a third promoter
sequence operably linked to said third
nucleotide sequence, whereby the third
nucleotide sequence is expressed by
said third virus in a suitable host;
and
- (d) a pharmaceutically acceptable carrier.

41. The vaccine formulation of claim 40 in
which the first fusion protein has the amino acid
sequence (SEQ ID NO:26) depicted in Figure 44, the

first promoter is modified p7.5, the second fusion protein has the amino acid sequence (SEQ ID NO:30) depicted in Figure 46, the second promoter is modified p7.5, the third nucleotide sequence encodes a protein
5 having the amino acid sequence (SEQ ID NO:10) depicted in Figure 24, and the third promoter is modified p7.5.

42. A vaccine formulation comprising:

- 10 (a) a first recombinant replicable vaccinia virus, the genome of which comprises
(i) a first nucleotide sequence encoding a first fusion protein, said first fusion protein comprising a hepatitis B virus core antigen or
15 derivative thereof displaying core antigenicity, fused at its carboxy terminus via a peptide bind to a hepatitis B virus preS1 region or derivative thereof displaying preS1
20 antigenicity, and (ii) a first promoter sequence operably linked to said first nucleotide sequence, whereby the first nucleotide sequence is expressed by said first virus in a suitable host;
- 25 (b) a second recombinant replicable vaccinia virus, the genome of which comprises (i) a second nucleotide sequence encoding a hepatitis B virus MS protein or a derivative thereof
30 displaying MS antigenicity, and (ii) a second promoter operably linked to said second nucleotide sequence, whereby the second nucleotide sequence is expressed by said second virus in a suitable
35 host; and

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(c) a pharmaceutically acceptable carrier.

43. The vaccine formulation of claim 42 in which the first fusion protein has the amino acid
5 sequence (SEQ ID NO:26) depicted in Figure 44, the first promoter is modified p7.5, the second nucleotide sequence encodes an MS protein having the sequence (SEQ ID NO:8) depicted in Figure 23, and in which a
10 sequence upstream of the second nucleotide sequence matches a consensus sequence associated with strong ribosome binding.

44. A vaccine formulation comprising:

- 15 (a) a first recombinant replicable vaccinia virus, the genome of which comprises
(i) a first nucleotide sequence encoding a first fusion protein, said first fusion protein comprising a
20 hepatitis B virus core antigen or derivative thereof displaying core antigenicity, fused at its carboxy terminus via a peptide bind to a hepatitis B virus preS2 region or derivative thereof displaying preS2
25 antigenicity, and (ii) a first promoter sequence operably linked to said first nucleotide sequence, whereby the first nucleotide sequence is expressed by said first virus in a suitable host;
- 30 (b) a second recombinant replicable vaccinia virus, the genome of which comprises (i) a second nucleotide sequence encoding a hepatitis B virus S protein or a derivative thereof
35 displaying S antigenicity, and (ii) a

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second promoter sequence operably
linked to said second nucleotide
sequence, whereby the second nucleotide
sequence is expressed by said second
virus in a suitable host; and

(c) a pharmaceutically acceptable carrier.

45. The vaccine formulation of claim 44 in
which the first fusion protein has the amino acid
sequence (SEQ ID NO:30) depicted in Figure 46, the
first promoter is modified p7.5, the second nucleotide
sequence encodes a protein having the amino acid
sequence (SEQ ID NO:10) depicted in Figure 24, and the
second promoter is modified p7.5.

15

46. A method of preventing hepatitis or
other undesirable consequence of hepatitis B virus
infection in a subject comprising administering to the
subject an effective amount of the recombinant virus
of claim 1.

20

47. A method of preventing hepatitis or
other undesirable consequence of hepatitis B virus
infection in a subject comprising administering to the
subject an effective amount of the recombinant virus
of claim 4.

25

48. A method of preventing hepatitis or
other undesirable consequence of hepatitis B virus
infection in a subject comprising administering to the
subject an effective amount of the recombinant virus
of claim 9.

30

49. A method of preventing hepatitis or
other undesirable consequence of hepatitis B virus

35

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infection in a subject comprising administering to the subject an effective amount of the recombinant virus of claim 10.

5 50. A method of preventing hepatitis or other undesirable consequence of hepatitis B virus infection in a subject comprising administering to the subject an effective amount of the recombinant virus of claim 15.

10

 51. A method of preventing hepatitis or other undesirable consequence of hepatitis B virus infection in a subject comprising administering to the subject an effective amount of the vaccine formulation
15 of claim 39.

 52. A method of preventing hepatitis or other undesirable consequence of hepatitis B virus infection in a subject comprising administering to the
20 subject an effective amount of the vaccine formulation of claim 40.

 53. A method of preventing hepatitis or other undesirable consequence of hepatitis B virus
25 infection in a subject comprising administering to the subject an effective amount of:

 (a) a first recombinant replicable vaccinia virus, the genome of which comprises
 (i) a first nucleotide sequence
30 encoding a first fusion protein, said first fusion protein comprising a hepatitis B virus core antigen or derivative thereof displaying core antigenicity, fused at its carboxy
35 terminus via a peptide bind to a

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- hepatitis B virus preS1 region or derivative thereof displaying preS1 antigenicity, and (ii) a first promoter sequence operably linked to said first nucleotide sequence, whereby the first nucleotide sequence is expressed by said first virus in a suitable host;
- 5
- (b) a second recombinant replicable vaccinia virus, the genome of which comprises (i) a second nucleotide sequence encoding a second fusion protein, said second fusion protein comprising a hepatitis B virus core antigen or derivative thereof
- 10
- displaying core antigenicity, fused at its carboxy terminus via a peptide bind to a hepatitis B virus preS2 region or derivative thereof displaying preS2 antigenicity, and (ii) a second
- 15
- promoter sequence operably linked to said second nucleotide sequence, whereby the second nucleotide sequence is expressed by said second virus in a suitable host; and
- 20
- (c) a third recombinant replicable vaccinia virus, the genome of which comprises (i) a third nucleotide sequence encoding a hepatitis B virus S protein or a derivative thereof displaying S antigenicity, and (ii) a third promoter
- 25
- sequence operably linked to said third nucleotide sequence, whereby the third nucleotide sequence is expressed by said third virus in a suitable host.
- 30
- 35

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54. A method of preventing hepatitis or other undesirable consequence of hepatitis B virus infection in a subject comprising administering to the subject an effective amount of:

- 5 (a) a first recombinant replicable vaccinia virus, the genome of which comprises
- (i) a first nucleotide sequence encoding a first fusion protein, said first fusion protein comprising a
- 10 hepatitis B virus core antigen or derivative thereof displaying core antigenicity, fused at its carboxy terminus via a peptide bind to a
- 15 hepatitis B virus preS1 region or derivative thereof displaying preS1 antigenicity, and (ii) a first promoter sequence operably linked to said first nucleotide sequence, whereby the first nucleotide sequence is expressed by
- 20 said first virus in a suitable host; and
- (b) a second recombinant replicable vaccinia virus, the genome of which comprises (i) a second nucleotide
- 25 sequence encoding a hepatitis B virus MS protein or a derivative thereof displaying MS antigenicity, and (ii) a second promoter operably linked to said second nucleotide sequence, whereby the
- 30 second nucleotide sequence is expressed by said second virus in a suitable host.

55. A method of preventing hepatitis or

35 other undesirable consequence of hepatitis B virus

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infection in a subject comprising administering to the subject an effective amount of:

- 5 (a) a first recombinant replicable vaccinia virus, the genome of which comprises
(i) a first nucleotide sequence
encoding a first fusion protein, said
first fusion protein comprising a
hepatitis B virus core antigen or
10 derivative thereof displaying core antigenicity, fused at its carboxy terminus via a peptide bond to a
hepatitis B virus preS2 region or
derivative thereof displaying preS2
15 antigenicity, and (ii) a first promoter sequence operably linked to said first nucleotide sequence, whereby the first nucleotide sequence is expressed by said first virus in a suitable host;
and
20 (b) a second recombinant replicable vaccinia virus, the genome of which comprises (i) a second nucleotide sequence encoding a hepatitis B virus S protein or a derivative thereof
25 displaying S antigenicity, and (ii) a second promoter sequence operably linked to said second nucleotide sequence, whereby the second nucleotide sequence is expressed by said second
30 virus in a suitable host.

56. A method of treating hepatitis or other undesirable consequence of hepatitis B virus infection comprising administering to a subject in need of such

35

treatment an effective amount of the recombinant vaccinia virus of claim 1.

57. A method of treating hepatitis or other
5 undesirable consequence of hepatitis B virus infection comprising administering to a subject in need of such treatment an effective amount of the recombinant vaccinia virus of claim 4.

10 58. A purified protein having the amino acid sequence (SEQ ID NO:13) depicted in Figure 30.

59. A purified nucleic acid encoding the
protein of claim 58.

15

20

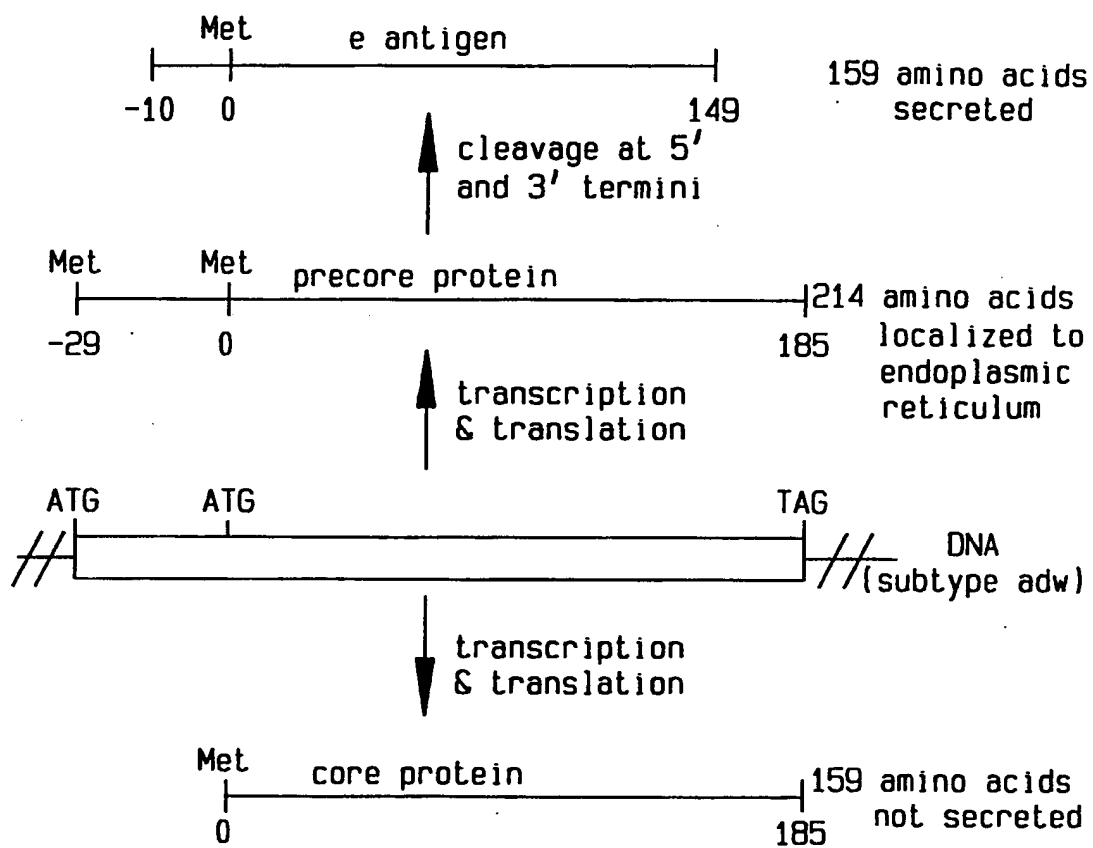
25

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FIG. 1



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		10		20		30		40		50		60	
1		ATAAATAATA		AATACAATAA		TTAATTTC		GTAAAAGTAG		AAAATATATT		CTAATTTATT	60
61		GCAC											64
		10		20		30		40		50		60	

FIG.2

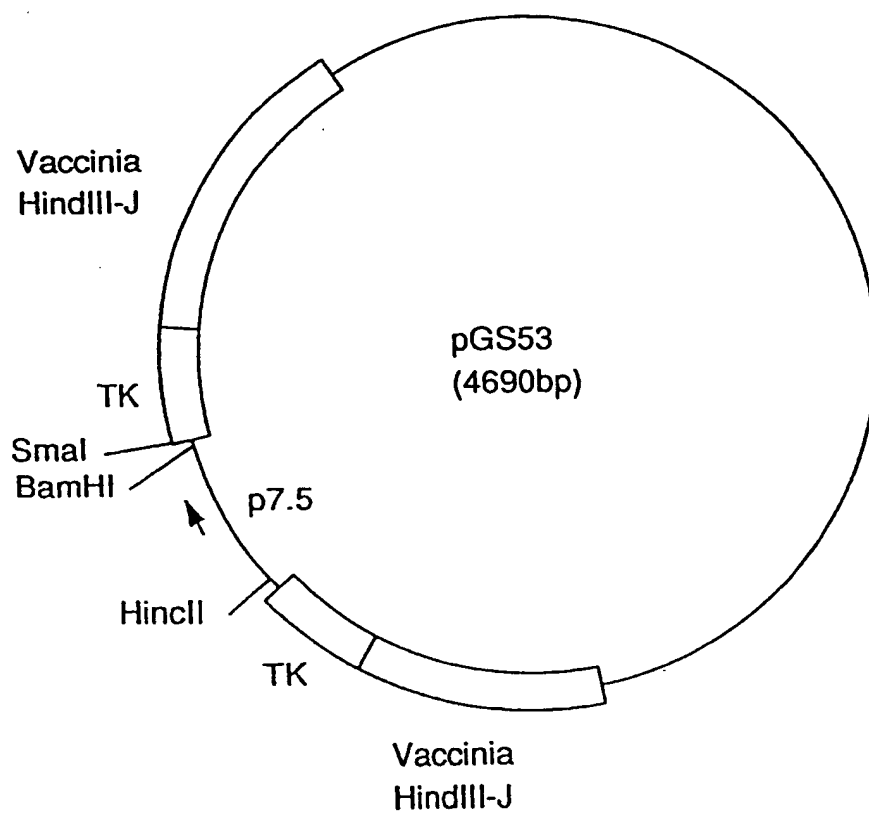
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1		CTAGAAGCGA		TGCTACGCTA		GTCACAATCA		CCACTTTCAT		ATTTAGAATA		TATGTATGTA	60
61		AAAATATAGT		AGAATTTTCAT		TTTGTTTTTT		TCTATGCTAT		AAAT			104
		10		20		30		40		50		60	

FIG.4

		10		20		30		40		50		60	
1		AAAAATTGAA		ATTTTATTTT		TTTTTTTTTGG		AATATAAATA		AG			42
		10		20		30		40		50		60	

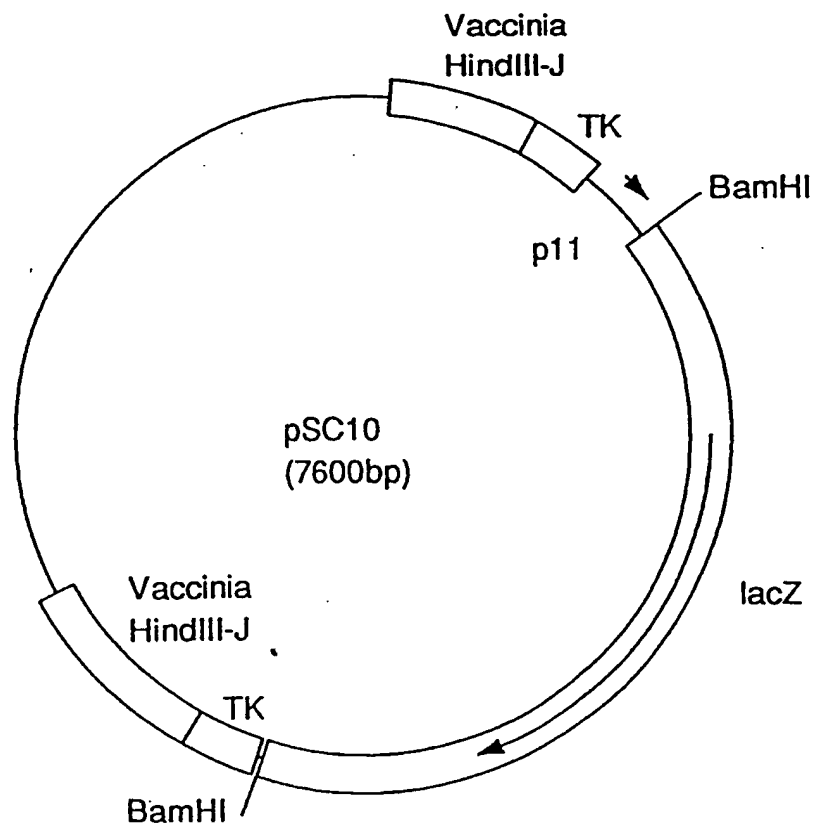
FIG.6

FIG. 3



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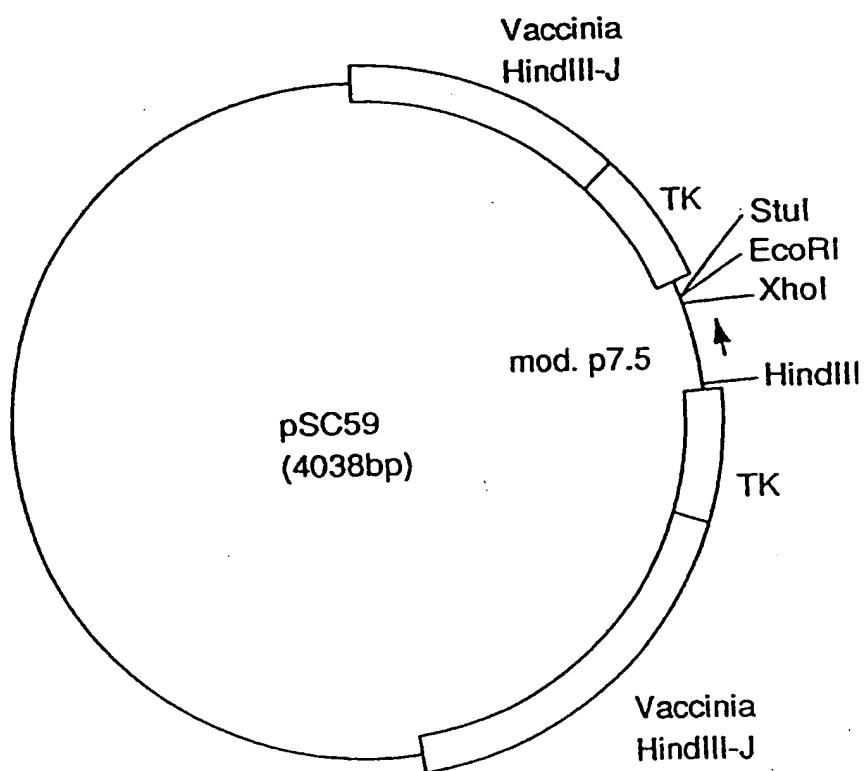
FIG. 5



SUBSTITUTE SHEET (RULE 26)

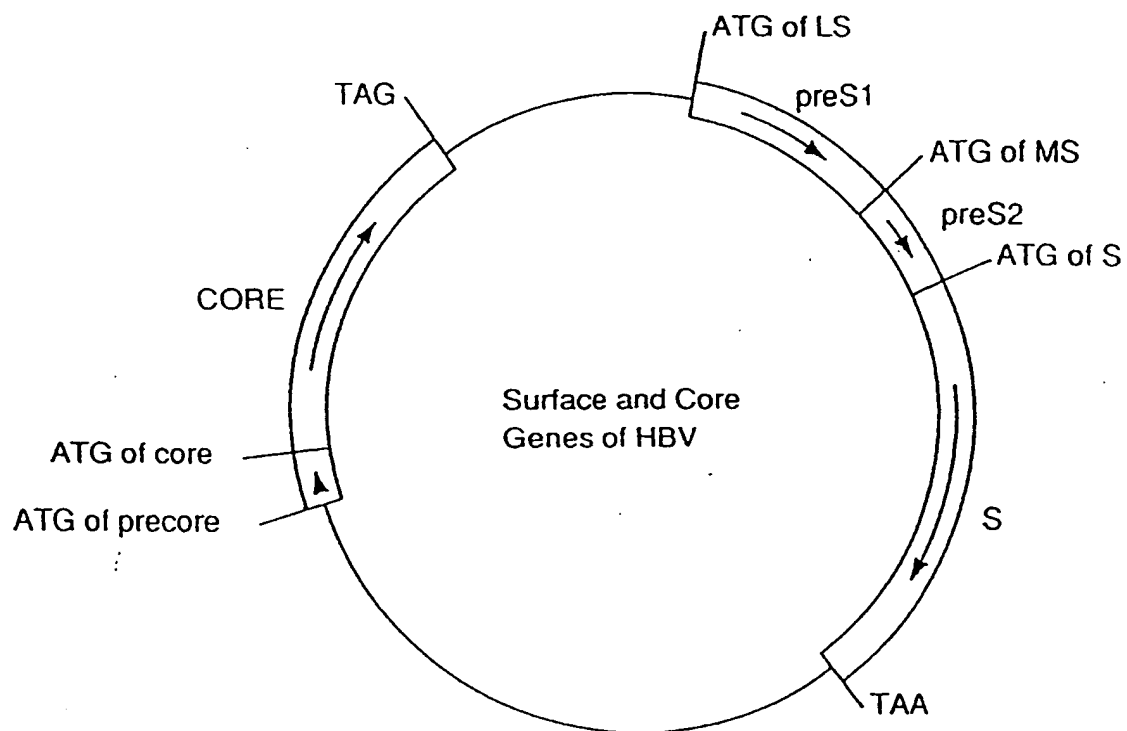
5/90

FIG. 7



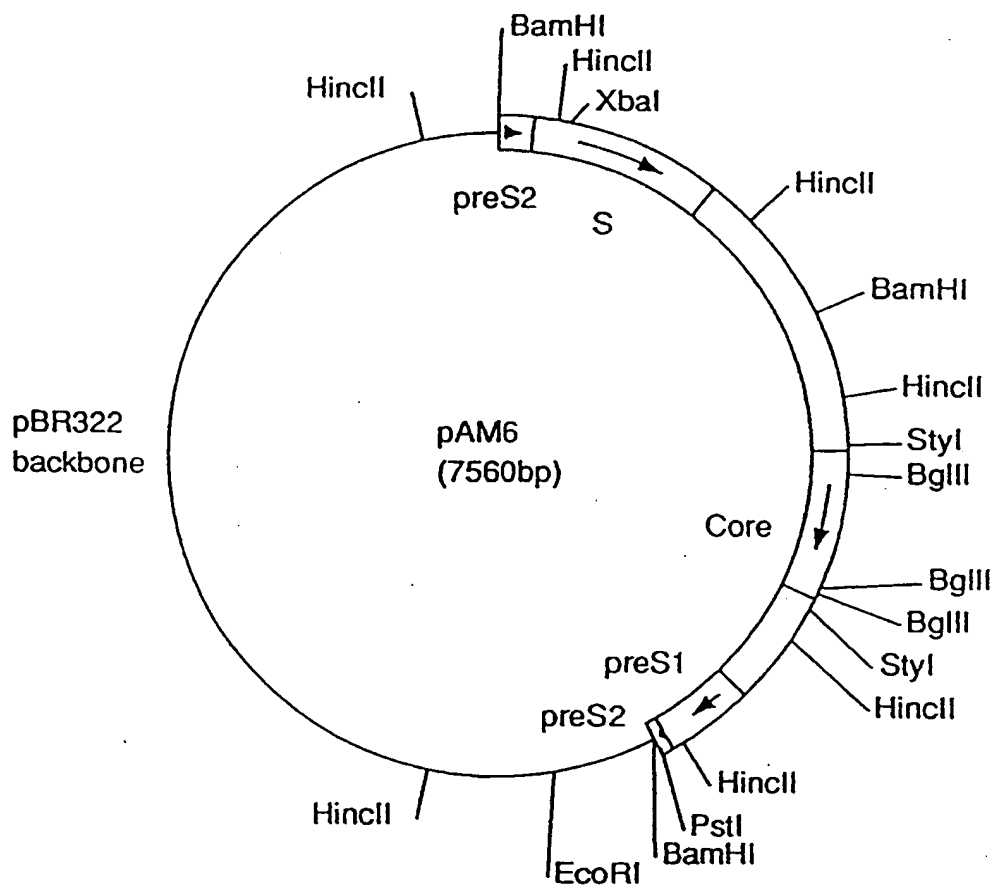
6/90

FIG. 8



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FIG. 9



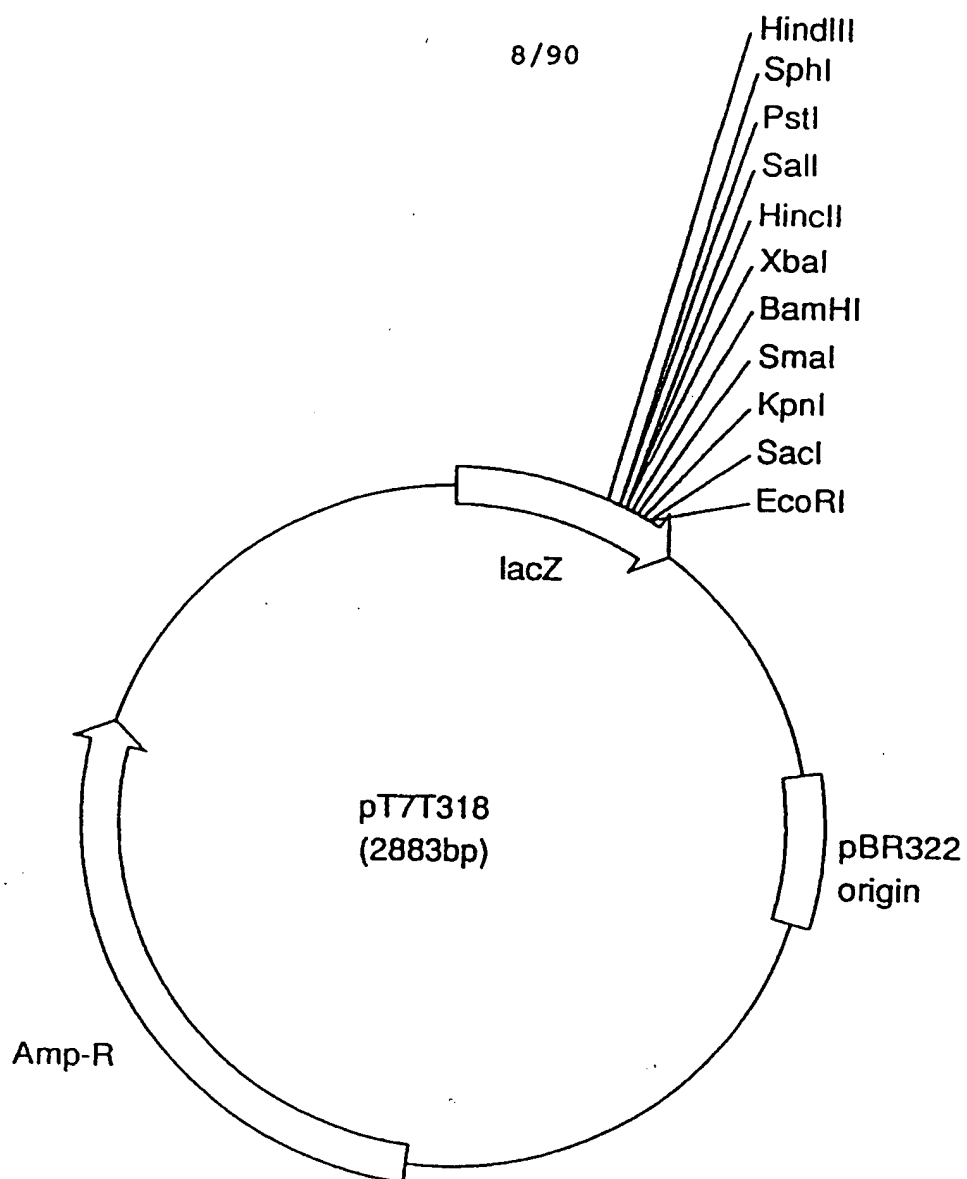
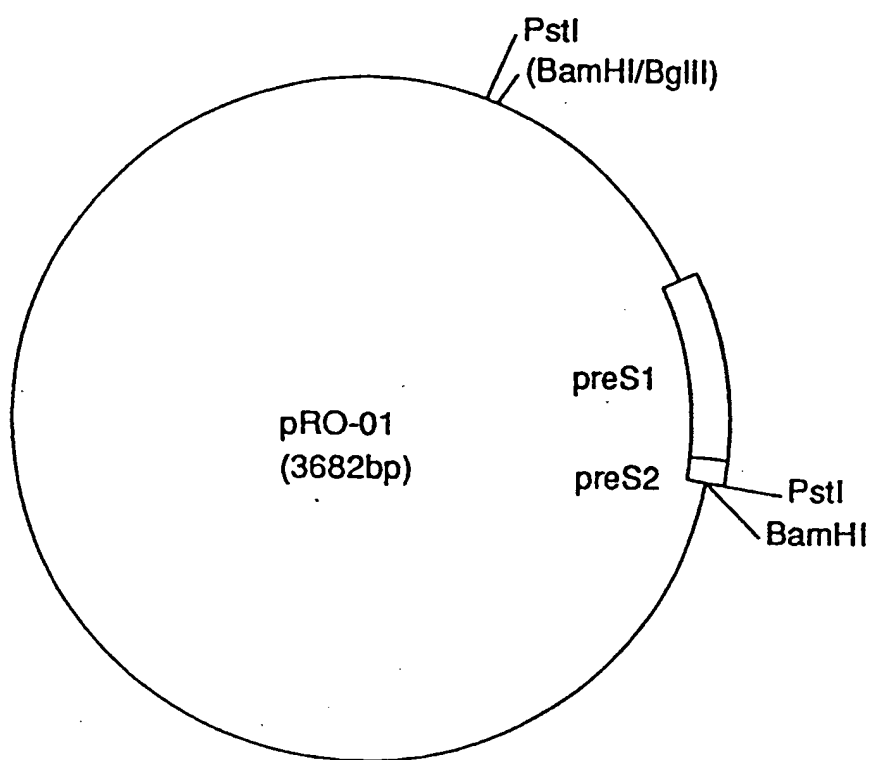


FIG. 10

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FIG. 11



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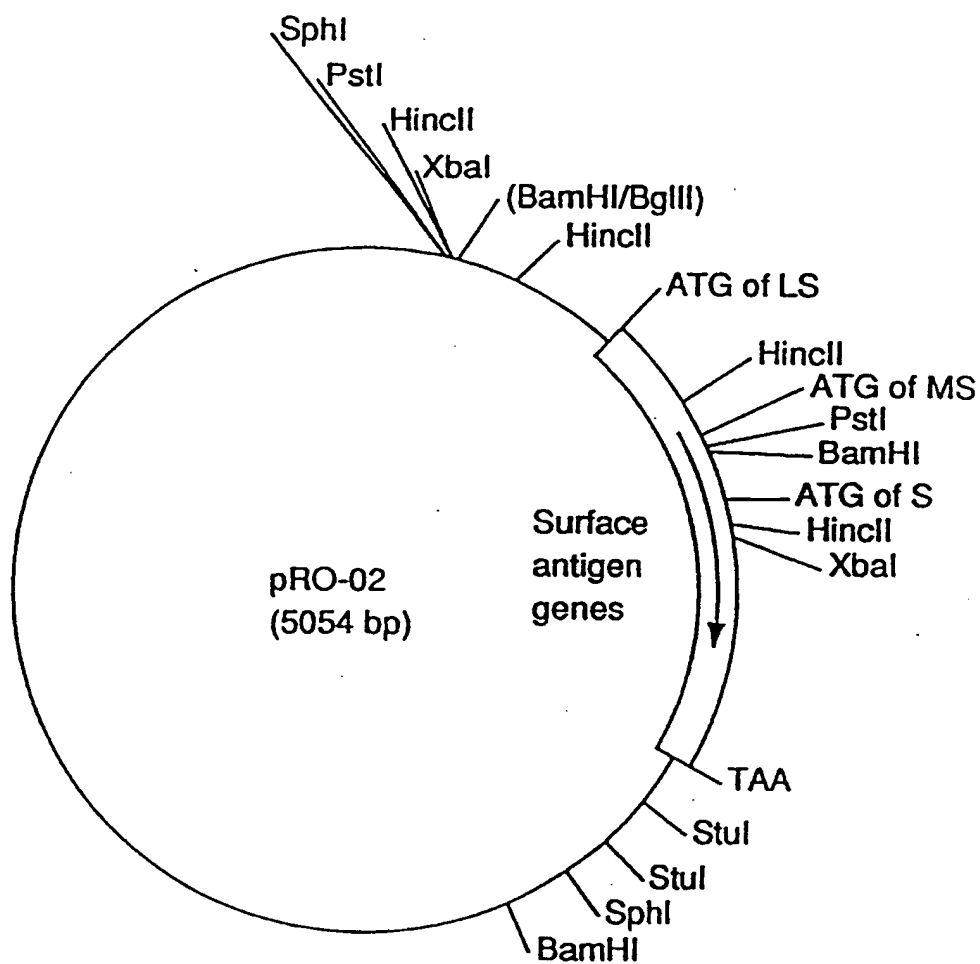
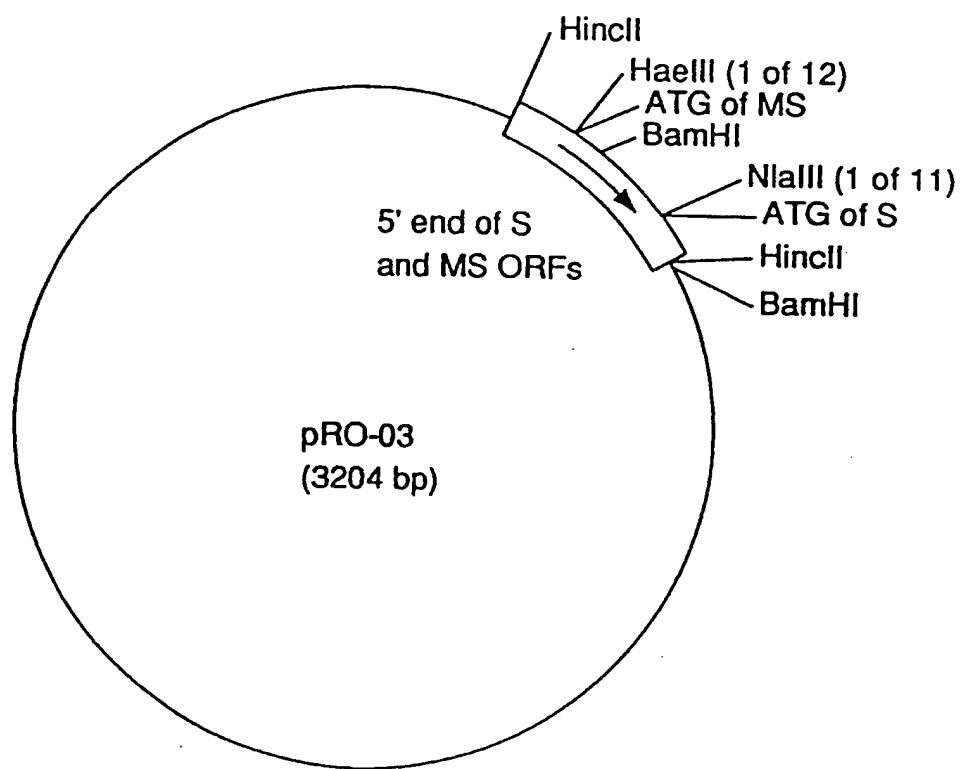


FIG. 12

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FIG. 13



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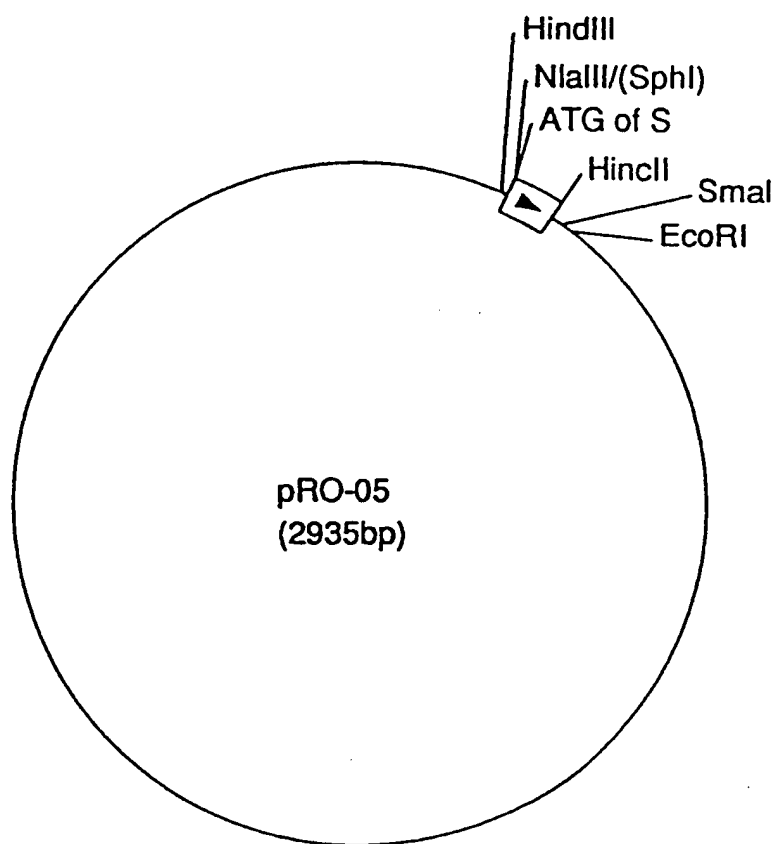


FIG. 14

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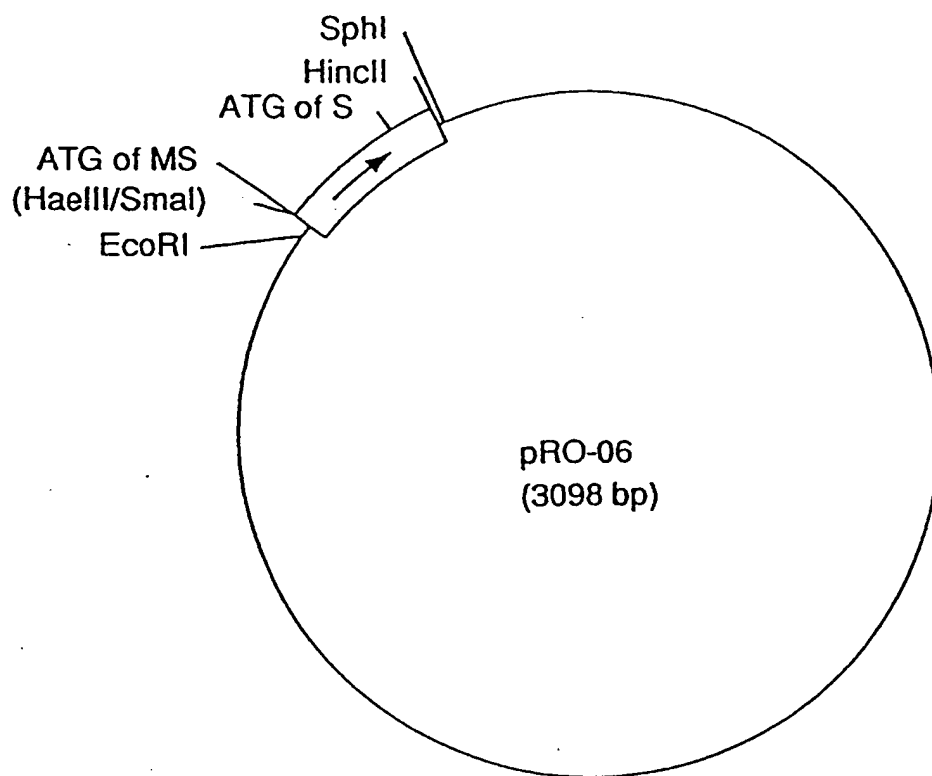


FIG. 15

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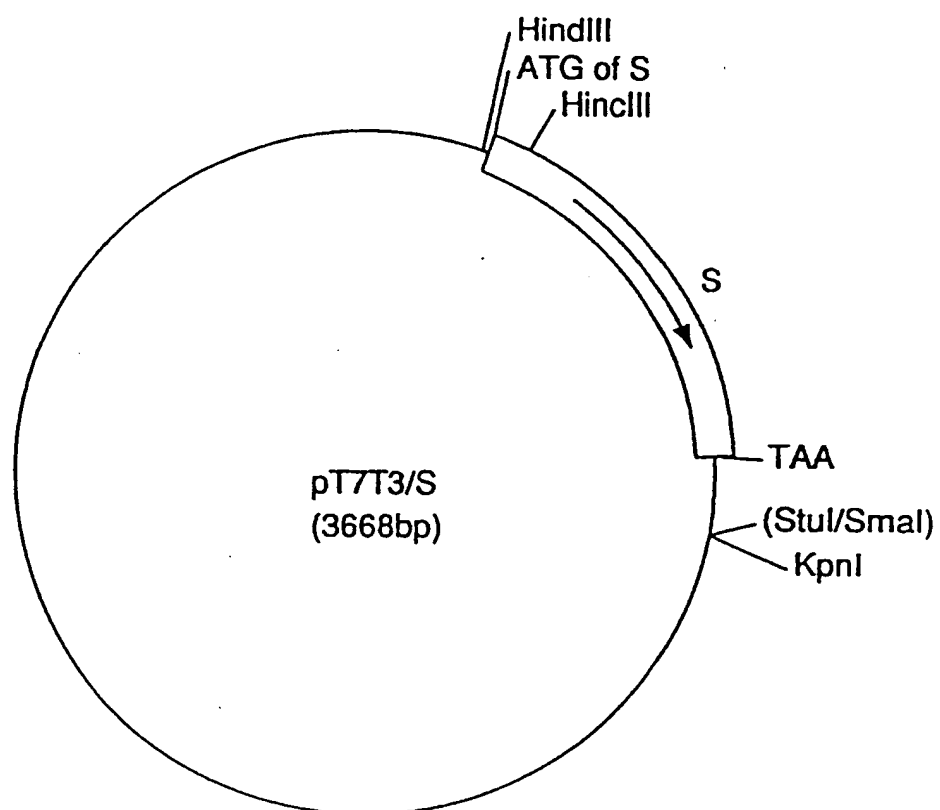
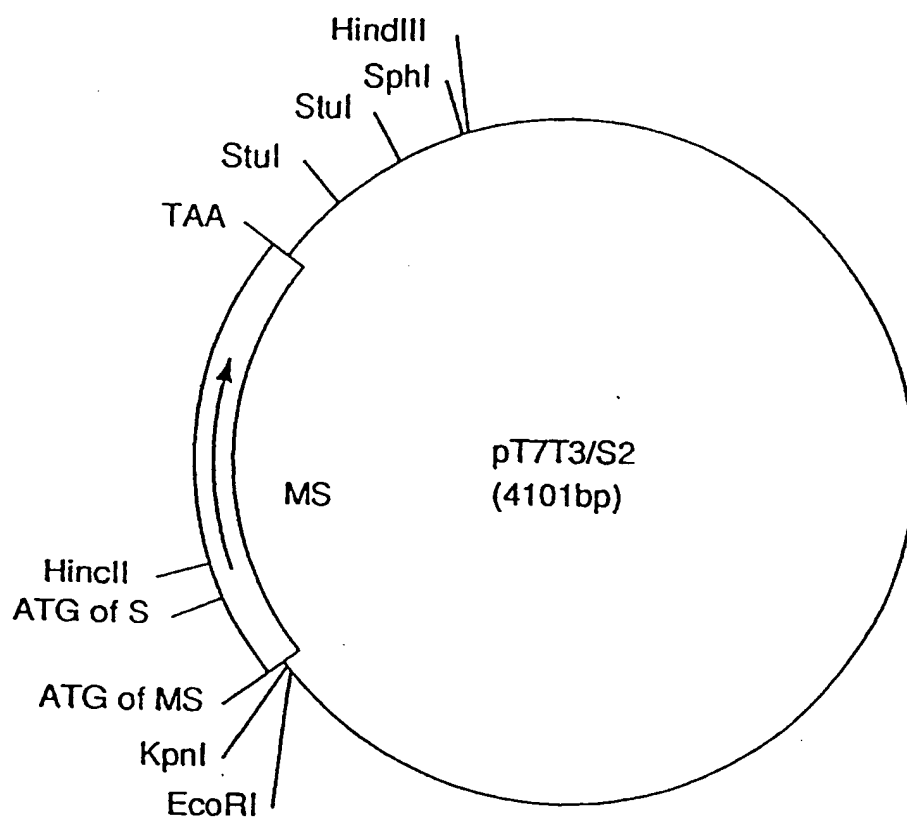


FIG. 16

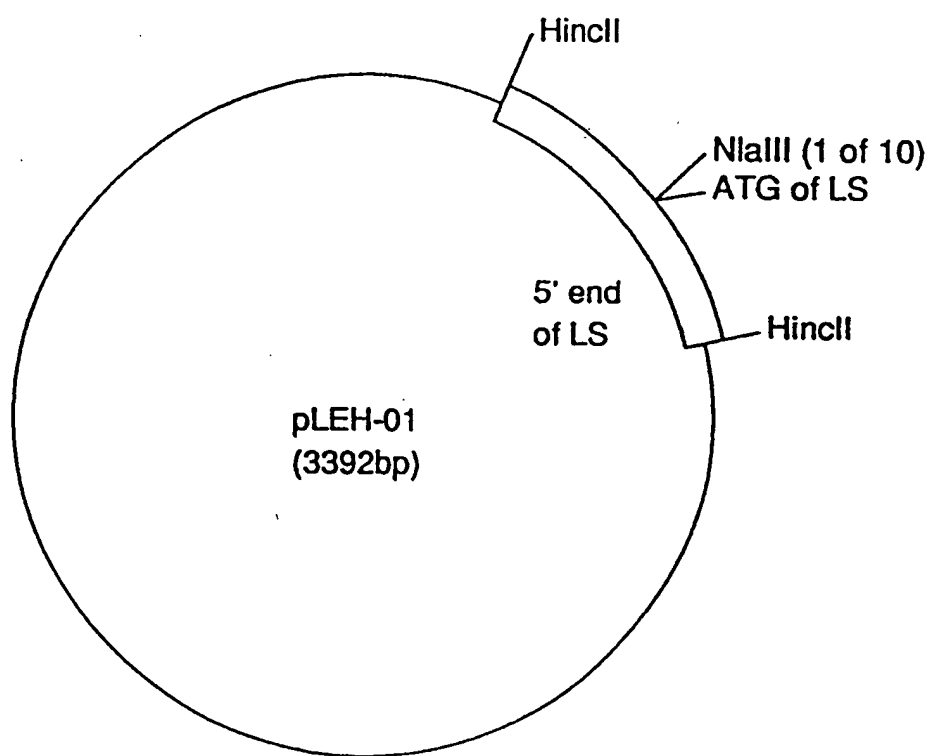
15/90

FIG. 17



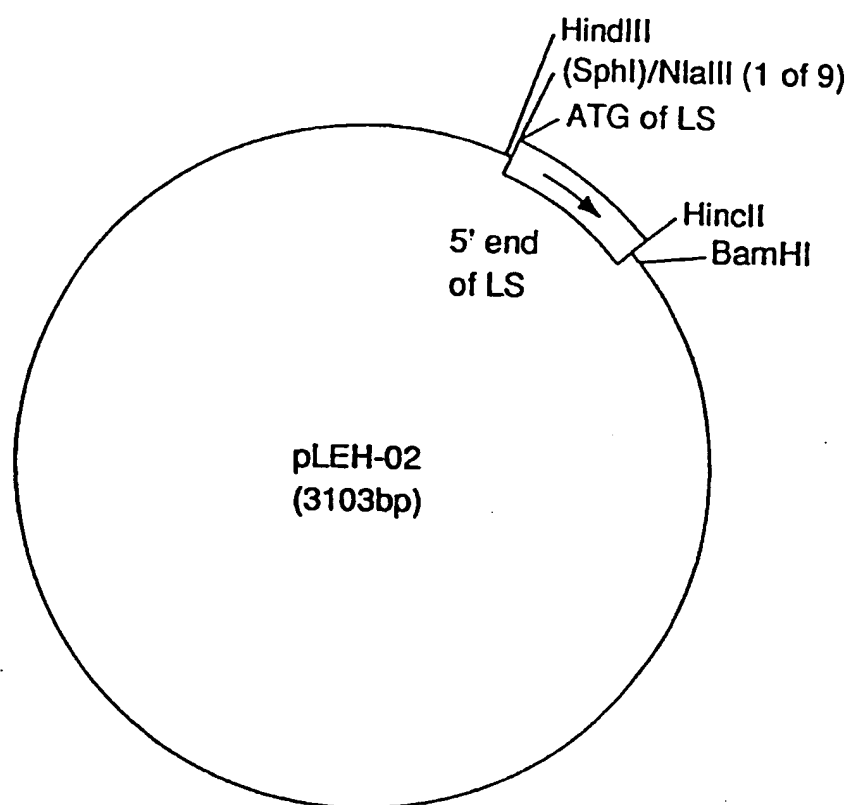
16/90

FIG. 18



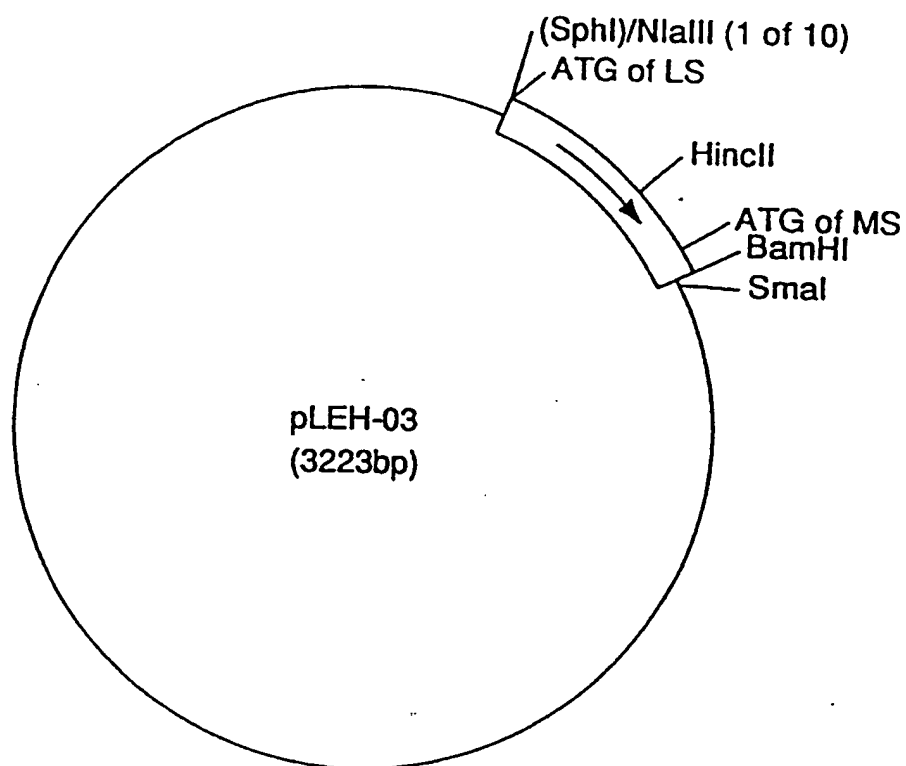
17/90

FIG. 19



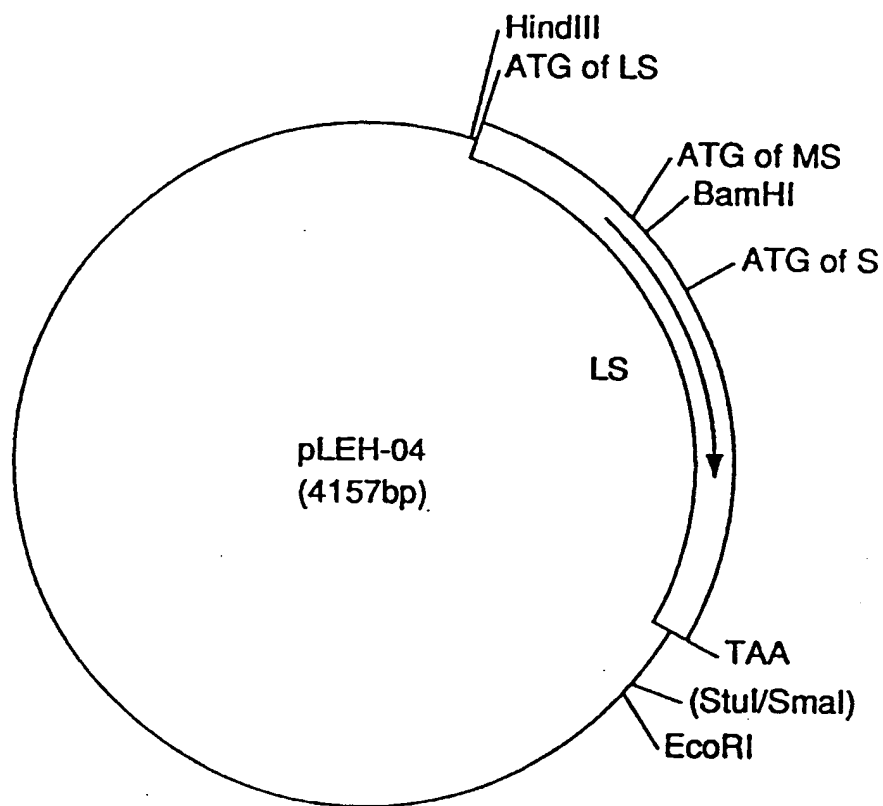
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FIG. 20



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FIG. 21



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1 / 1 31 / 11
ATG GGG ACG AAT CTT TCT GTT CCC AAT CCT CTG GGA TTC LTT CCC GAT CAT CAG TTG GAC
met gly thr asn leu ser val pro asn pro leu gly phe phe pro asp his gln leu asp
61 / 21 91 / 31
CCT GCA TTC GGA GCC AAC TCA Aac AAT CCA GAT TGG GAC TTC AAC CCC ATC AAG GAC CAC
pro ala phe gly ala asn ser asn asn pro asp trp asp phe asn pro ile lys asp his
121 / 41 151 / 51
TGG CCA GCA GCC AAC CAG GTA GGA GTG GGA GCA TTC GGG CCA GGG LTC ACC CCT CCA CAC
trp pro ala ala asn gln val gly val gly ala phe gly pro gly phe thr pro pro his
181 / 61 211 / 71
GGC GGT gTT TTG GGG TGG AGC CCT CAG GCT CAG GGC ATA TTG ACC ACA GTG TCA ACA ATT
gly gly val leu gly trp ser pro gln ala gln gly ile leu thr thr val ser thr ile
241 / 81 271 / 91
CCT CCT CCT GCC TCC ACC AAT CCG CAG TCA GGA AGG CAG CCT ACT CCC ATC TCT CCA CCT
pro pro pro ala ser thr asn arg gln ser gly arg gln pro thr pro ile ser pro pro
301 / 101 331 / 111
CTA AGA GAC AGT CAT CCT CAG GCC ATG CAG TGG AAc TCC ACT GCC TTe CAC CAA GCT CTG
leu arg asp ser his pro gln ala met gln trp asn ser thr ala phe his gln ala leu
361 / 121 391 / 131
CAG GAT CCC AGA GTC AGG GGT CTG TAT LTT CCT GCT GGT GGC TCC AGT TCA GGA ACA GTA
gln asp pro arg val arg gly leu tyr phe pro ala gly gly ser ser ser gly thr val
421 / 141 451 / 151
AAC CCT GCT CCG AAT ATT GCC TCT CAC ATC TCG TCA ATC TCC GCG AGG ACT GGG GAC CCT
asn pro ala pro asn ile ala ser his ile ser ser ile ser ala arg thr gly asp pro
481 / 161 511 / 171
GTG ACG AAc ATG GAG AAC ATC ACA TCA GGA TTC CTA GGA CCC CTG CTC GTG TTA CAG GCG
val thr asn met glu asn ile thr ser gly phe leu gly pro leu leu val leu gln ala
541 / 181 571 / 191
GGG TTT TTC TTG TTG ACA AGA ATC CTC ACA ATA CCG CAG AGT CTA GAC TCG TGG TGG ACT
gly phe phe leu leu thr arg ile leu thr ile pro gln ser leu asp ser trp trp thr
601 / 201 631 / 211
TCT CTC AAT TTT CTA GGG GGA TCA CCC GTG TGT CTT GGC CAA AAT TCG CAG TCC CCA ACC
ser leu asn phe leu gly gly ser pro val cys leu gly gln asn ser gln ser pro thr
661 / 221 691 / 231
TCC AAT CAC TCA CCA ACC TCC TGT CCT CCA ATT TGT CCT GGT TAT CGC TGG ATG TGT CTG
ser asn his ser pro thr ser cys pro pro ile cys pro gly tyr arg trp met cys leu
721 / 241 751 / 251
CGG CGT TTT ATC ATA TTC CTC TTC ATC CTG CTG CTA TGC CTC ATC TTC TTA TTG GTT CTT
arg arg phe ile ile phe leu phe ile leu leu leu cys leu ile phe leu leu val leu

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FIG.22A

SUBSTITUTE SHEET (RULE 26)

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781 / 261	811 / 271
CTG GAT TAT CAA GGT ATG TTG CCC GTT TGT CCT CTA ATT CCA GGA TCA ACA ACA ACC AGT	
leu asp tyr gln gly met leu pro val cys pro leu ile pro gly ser thr thr thr ser	
841 / 281	871 / 291
ACG GGA CCA TGC AAA ACC TGC ACG ACT CCT GCT CAA GGC AAC TCT ATG TTT CCC TCA TGT	
thr gly pro cys lys thr cys thr thr pro ala gln gly asn ser met phe pro ser cys	
901 / 301	931 / 311
TGC TGT ACA AAA CCT ACG GAT GGA AAT TGC ACC TGT ATT CCC ATC CCA TCG TCT TGG GCT	
cys cys thr lys pro thr asp gly asn cys thr cys ile pro ile pro ser ser trp ala	
961 / 321	991 / 331
TTC GCA AAA TAC CTA TGG GAG TGG GCC TCA GTC CGT TTC TCT TGG CTC AGT TTA CTA GTG	
phe ala lys tyr leu trp glu trp ala ser val arg phe ser trp leu ser leu leu val	
1021 / 341	1051 / 351
CCA TTT GTT CAG TGG TTC GTA GGG CTT TCC CCC ACT GTT TGG CTT TCA GCT ATA TGG ATG	
pro phe val gln trp phe val gly leu ser pro thr val trp leu ser ala ile trp met	
1081 / 361	1111 / 371
ATG TGG TAT TGG GGG CCA AGT CTG TAC AGC ATC GTG AGT CCC TTT ATA CCG CTG TTA CCA	
met trp tyr trp gly pro ser leu tyr ser ile val ser pro phe ile pro leu leu pro	
1141 / 381	
ATT TTC TTT TGT CTC TGG GTA TAC ATT TAA	
ile phe phe cys leu trp val tyr ile OCH	

FIG.22B

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1 / 1 31 / 11
ATG CAG TGG AAC TCC ACT GCC TTC CAC CAA GCT CTG CAG GAT CCC AGA GTC AGG GGT CTG
met gln trp asn ser thr ala phe his gln ala leu gln asp pro arg val arg gly leu
61 / 21 91 / 31
TAT TTT CCT GCT GGT GGC TCC AGT TCA GGA ACA GTA AAC CCT GCT CCG AAT ATT GCC TCT
tyr phe pro ala gly gly ser ser ser gly thr val asn pro ala pro asn ile ala ser
121 / 41 151 / 51
CAC ATC TCG TCA ATC TCC GCG AGG ACT GGG GAC CCT GTG ACG AAC ATG GAG AAC ATC ACA
his ile ser ser ile ser ala arg thr gly asp pro val thr asn met glu asn ile thr
181 / 61 211 / 71
TCA GGA TTC CTA GGA CCC CTG CTC GTG TTA CAG GCG GGG TTT TTC TTG TTG ACA AGA ATC
ser gly phe leu gly pro leu leu val leu gln ala gly phe phe leu leu thr arg ile
241 / 81 271 / 91
CTC ACA ATA CCG CAG AGT CTA GAC TCG TGG TGG ACT TCT CTC AAT TTT CTA GGG GGA TCA
leu thr ile pro gln ser leu asp ser trp trp thr ser leu asn phe leu gly gly ser
301 / 101 331 / 111
CCC GTG TGT CTT GGC CAA AAT TCG CAG TCC CCA ACC TCC AAT CAC TCA CCA ACC TCC TGT
pro val cys leu gly gln asn ser gln ser pro thr ser asn his ser pro thr ser cys
361 / 121 391 / 131
CCT CCA ATT TGT CCT GGT TAT CCG TGG ATG TGT CTG CCG CGT TTT ATC ATA TTC CTC TTC
pro pro ile cys pro gly tyr arg trp met cys leu arg arg phe ile ile phe leu phe
421 / 141 451 / 151
ATC CTG CTG CTA TGC CTC ATC TTC TTA TTG GTT CTT CTG GAT TAT CAA GGT ATG TTG CCC
ile leu leu leu cys leu ile phe leu leu val leu leu asp tyr gln gly met leu pro
481 / 161 511 / 171
GTT TGT CCT CTA ATT CCA GGA TCA ACA ACA ACC AGT ACG GGA CCA TGC AAA ACC TGC ACG
val cys pro leu ile pro gly ser thr thr thr ser thr gly pro cys lys thr cys thr
541 / 181 571 / 191
ACT CCT GCT CAA GGC AAC TCT ATG TTT CCC TCA TGT TGC TGT ACA AAA CCT ACG GAT GGA
thr pro ala gln gly asn ser met phe pro ser cys cys cys thr lys pro thr asp gly
601 / 201 631 / 211
AAT TGC ACC TGT ATT CCC ATC CCA TCG TCT TGG GCT TTC GCA AAA TAC CTA TGG GAG TGG
asn cys thr cys ile pro ile pro ser ser trp ala phe ala lys tyr leu trp glu trp
661 / 221 691 / 231
GCC TCA GTC CGT TTC TCT TGG CTC AGT TTA CTA GTG CCA TTT GTT CAG TGG TTC GTA GGG
ala ser val arg phe ser trp leu ser leu leu val pro phe val gln trp phe val gly
721 / 241 751 / 251
CTT TCC CCC ACT GTT TGG CTT TCA GCT ATA TGG ATG ATG TGG TAT TGG GGG CCA AGT CTG
leu ser pro thr val trp leu ser ala ile trp met met trp tyr trp gly pro ser leu
781 / 261 811 / 271
TAC AGC ATC GTG AGT CCC TTT ATA CCG CTG TTA CCA ATT TTC TTT TGT CTC TGG GTA TAC
tyr ser ile val ser pro phe ile pro leu leu pro ile phe phe cys leu trp val tyr
841 / 281
ATT TAA
ile OCH

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FIG.23
SUBSTITUTE SHEET (RULE 26)

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1 / 1 31 / 11
ATG GAG AAC ATC ACA TCA GGA TTC CTA GGA CCC CTG CTC GTG TTA CAG GCG GGG TTT TTC
met glu asn ile thr ser gly phe leu gly pro leu leu val leu gln ala gly phe phe
61 / 21 91 / 31
TTG TTG ACA AGA ATC CTC ACA ATA CCG CAG AGT CTA GAC TCG TGG TGG ACT TCT CTC AAT
leu leu thr arg ile leu thr ile pro gln ser leu asp ser trp trp thr ser leu asn
121 / 41 151 / 51
TTT CTA GGG GGA TCA CCC GTG TGT CTT GGC CAA AAT TCG CAG TCC CCA ACC TCC AAT CAC
phe leu gly gly ser pro val cys leu gly gln asn ser gln ser pro thr ser asn his
181 / 61 211 / 71
TCA CCA ACC TCC TGT CCT CCA ATT TGT CCT GGT TAT CCG TGG ATG TGT CTG CCG CGT TTT
ser pro thr ser cys pro pro ile cys pro gly tyr arg trp met cys leu arg arg phe
241 / 81 271 / 91
ATC ATA TTC CTC TTC ATC CTG CTG CTA TGC CTC ATC TTC TTA TTG GTT CTT CTG GAT TAT
ile ile phe leu phe ile leu leu leu cys leu ile phe leu leu val leu leu asp tyr
301 / 101 331 / 111
CAA GGT ATG TTG CCC GTT TGT CCT CTA ATT CCA GGA TCA ACA ACA ACC AGT ACG GGA CCA
gln gly met leu pro val cys pro leu ile pro gly ser thr thr thr ser thr gly pro
361 / 121 391 / 131
TGC AAA ACC TGC ACG ACT CCT GCT CAA GGC AAC TCT ATG TTT CCC TCA TGT TGC TGT ACA
cys lys thr cys thr thr pro ala gln gly asn ser met phe pro ser cys cys thr
421 / 141 451 / 151
AAA CCT ACG GAT GGA AAT TGC ACC TGT ATT CCC ATC CCA TCG TCT TGG GCT TTC GCA AAA
lys pro thr asp gly asn cys thr cys ile pro ile pro ser ser trp ala phe ala lys
481 / 161 511 / 171
TAC CTA TGG GAG TGG GCC TCA GTC CGT TTC TCT TGG CTC AGT TTA CTA GTC CCA TTT GTT
tyr leu trp glu trp ala ser val arg phe ser trp leu ser leu leu val pro phe val
541 / 181 571 / 191
CAG TGG TTC GTA GGG CTT TCC CCC ACT GTT TGG CTT TCA GCT ATA TGG ATG ATG TGG TAT
gln trp phe val gly leu ser pro thr val trp leu ser ala ile trp met met trp tyr
601 / 201 631 / 211
TGG GGG CCA AGT CTG TAC AGC ATC GTG AGT CCC TTT ATA CCG CTG TTA CCA ATT TTC TTT
trp gly pro ser leu tyr ser ile val ser pro phe ile pro leu leu pro ile phe phe
661 / 221
TGT CTC TGG GTA TAC ATT TAA
cys leu trp val tyr ile OCH

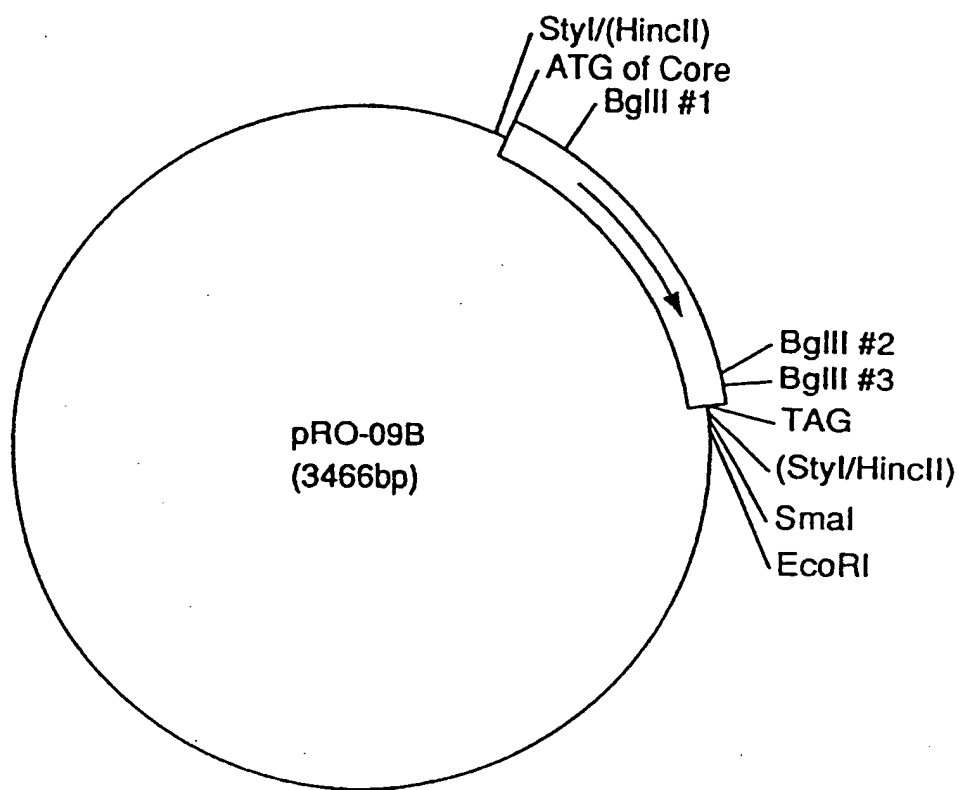
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FIG.24

SUBSTITUTE SHEET (RULE 26)

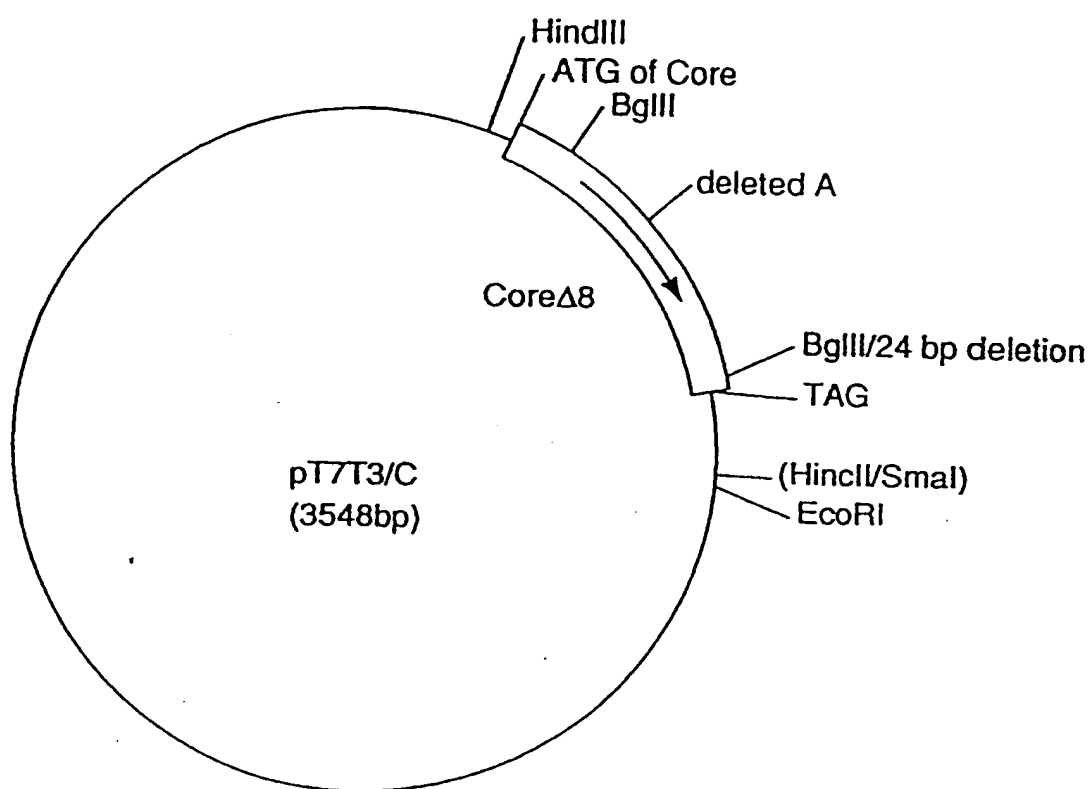
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FIG. 25



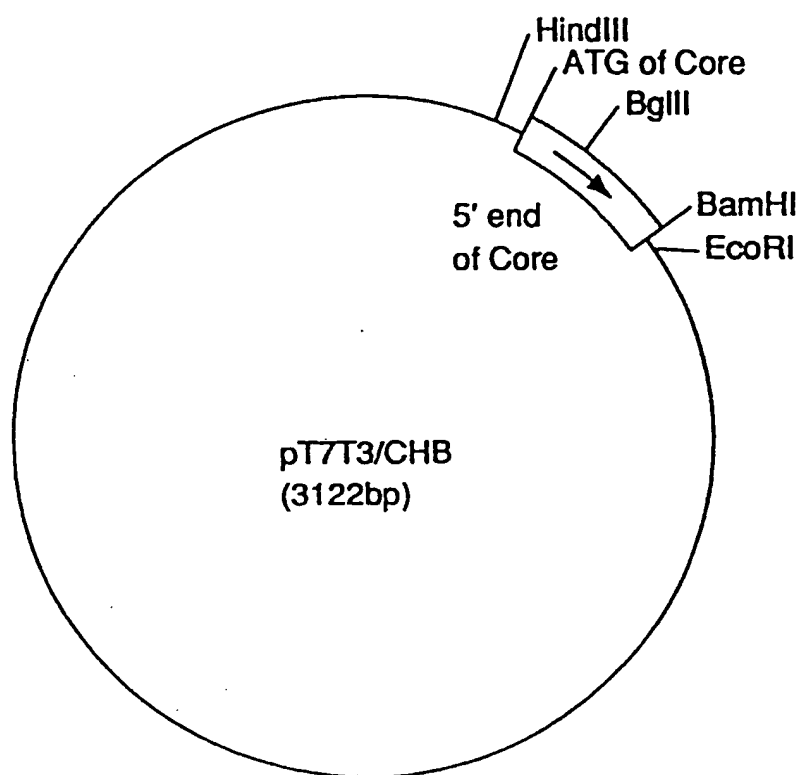
25/90

FIG. 26



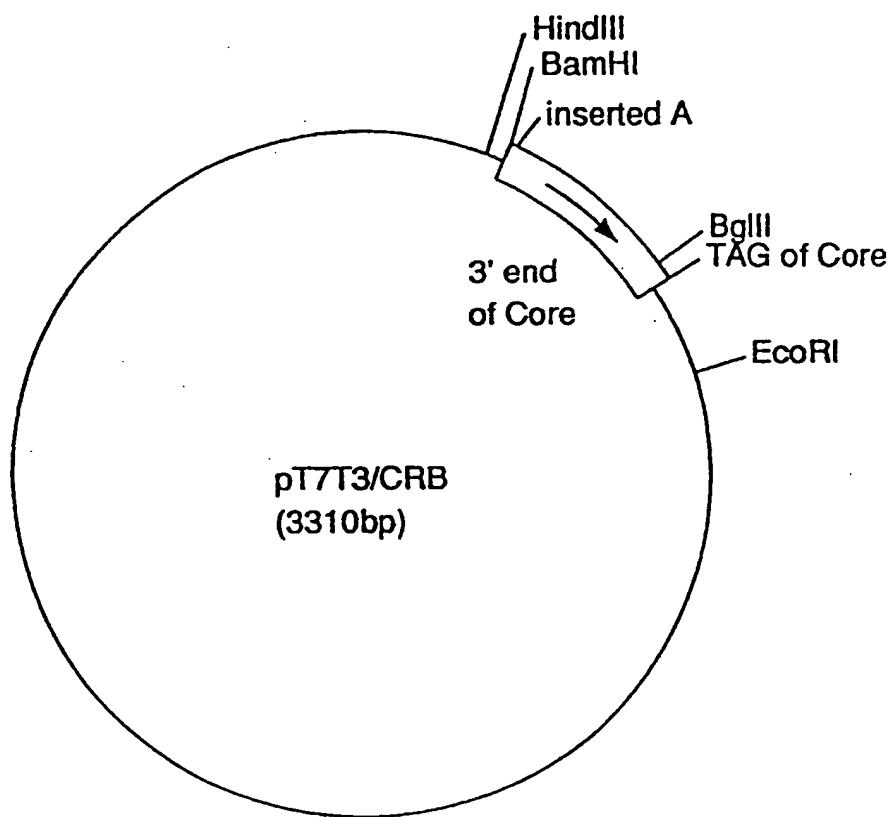
26/90

FIG. 27



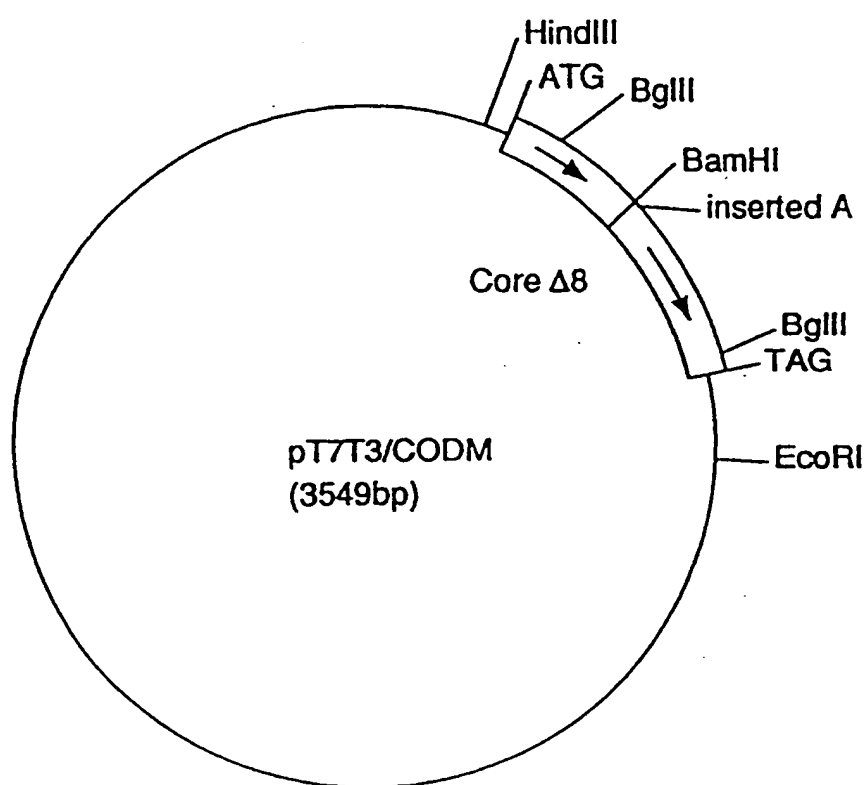
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FIG. 28



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FIG. 29



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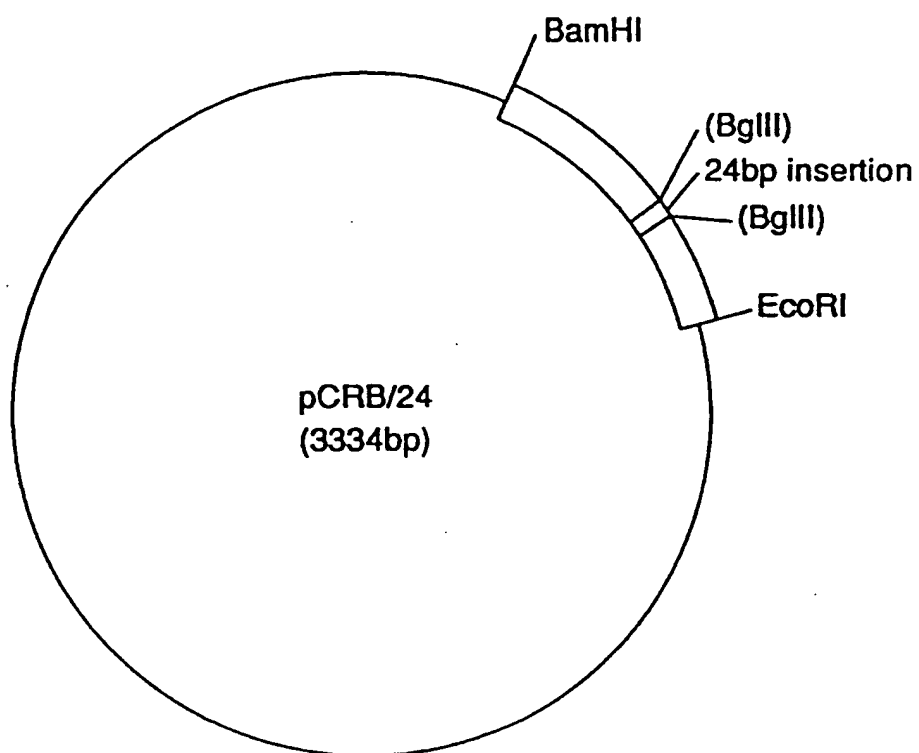
1 / 1	31 / 11
ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC TCG TTT TTG CCT	
met asp ile asp pro tyr lys glu phe gly ala thr val glu leu leu ser phe leu pro	
61 / 21	91 / 31
TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC ACC GCC TCA GCT CTG TAT CCG GAA	
ser asp phe phe pro ser val arg asp leu leu asp thr ala ser ala leu tyr arg glu	
121 / 41	151 / 51
GCC TTA GAG TCT CCT GAG CAT TGC TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC	
ala leu glu ser pro glu his cys ser pro his his thr ala leu arg gln ala ile leu	
181 / 61	211 / 71
TGC TGG GGG GAA TTG ATG ACT CTA GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA	
cys trp gly glu leu met thr leu ala thr trp val gly asn asn leu glu asp pro ala	
241 / 81	271 / 91
TCA AGG GAT CTA GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA ATT AGG CAA CTA	
ser arg asp leu val val asn tyr val asn thr asn met gly leu lys ile arg gln leu	
301 / 101	331 / 111
TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA GAG ACT GTA CTT GAA TAT TTG GTA	
leu trp phe his ile ser cys leu thr phe gly arg glu thr val leu glu tyr leu val	
361 / 121	391 / 131
TCT TTC GGA GTG TGG ATT CGC ACT CCT CCA GCC TAT AGA CCA CCA AAT GCC CCT ATC TTA	
ser phe gly val trp ile arg thr pro pro ala tyr arg pro pro asn ala pro ile leu	
421 / 141	451 / 151
TCA ACA CTT CCG GAA ACT ACT GTT GTT AGA CGA CCG GAC CGA GGC AGG TCC CCT AGA AGA	
ser thr leu pro glu thr thr val val arg arg arg asp arg gly arg ser pro arg arg	
481 / 161	511 / 171
AGA ACT CCC TCG CCT CGC AGA CGC AGA TCT CAA TCT CCG GAA TCT CAA TGT TAG	
arg thr pro ser pro arg arg arg ser gln ser arg glu ser gln cys AMB	

FIG.30

SUBSTITUTE SHEET (RULE 26)

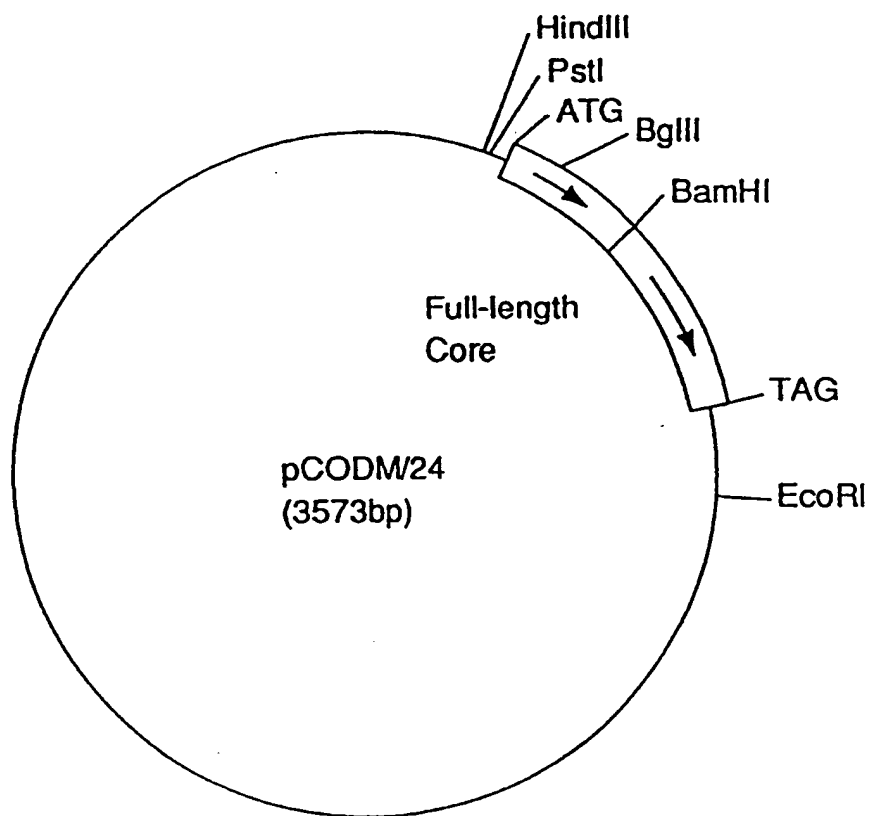
30/90

FIG. 31



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FIG. 32



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1 / 1 31 / 11
ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC TCG TTT TTG CCT
met asp ile asp pro tyr lys glu phe gly ala thr val glu leu leu ser phe leu pro
61 / 21 91 / 31
TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC ACC GCC TCA GCT CTG TAT CCG GAA
ser asp phe phe pro ser val arg asp leu leu asp thr ala ser ala leu tyr arg glu
121 / 41 151 / 51
GCC TTA GAG TCT CCT GAG CAT TGC TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC
ala leu glu ser pro glu his cys ser pro his his thr ala leu arg gln ala ile leu
181 / 61 211 / 71
TGC TGG GGG GAA TTG ATG ACT CTA GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA
cys trp gly glu leu met thr leu ala thr trp val gly asn asn leu glu asp pro ala
241 / 81 271 / 91
TCA AGG GAT CTA GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA ATT AGG CAA CTA
ser arg asp leu val val asn tyr val asn thr asn met gly leu lys ile arg gln leu
301 / 101 331 / 111
TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA GAG ACT GTA CTT GAA TAT TTG GTA
leu trp phe his ile ser cys leu thr phe gly arg glu thr val leu glu tyr leu val
361 / 121 391 / 131
TCT TTC GGA GTG TGG ATT CCG ACT CCT CCA GCC TAT AGA CCA CCA AAT GCC CCT ATC TTA
ser phe gly val trp ile arg thr pro pro ala tyr arg pro pro asn ala pro ile leu
421 / 141 451 / 151
TCA ACA CTT CCG GAA ACT ACT GTT GTT AGA CGA CCG GAC CGA GCC AGG TCC CCT AGA AGA
ser thr leu pro glu thr thr val val arg arg arg asp arg gly arg ser pro arg arg
481 / 161 511 / 171
AGA ACT CCC TCG CCT CCG AGA CCG AGA tcc caa tcc ccg cgt cgc ogo cga TCT CAA TCT
ogo thr pro ser pro arg arg arg arg ser gln ser pro arg arg arg arg ser gln ser
541 / 181
CCG GAA TCT CAA TGT TAG
arg glu ser gln cys AMB

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FIG.33

SUBSTITUTE SHEET (RULE 26)

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FIG. 34

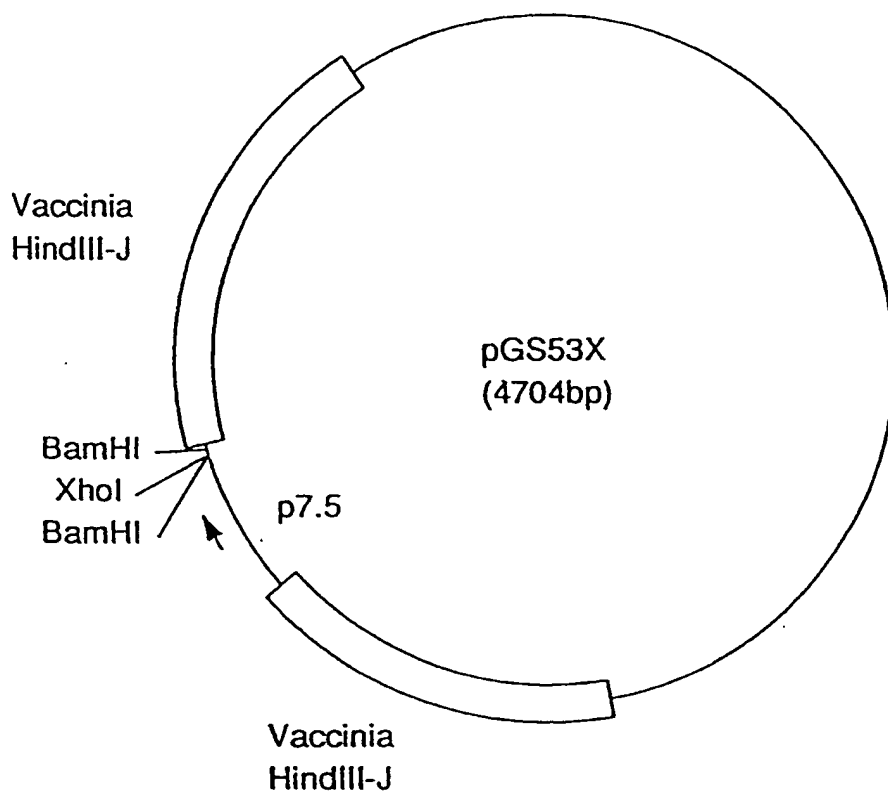
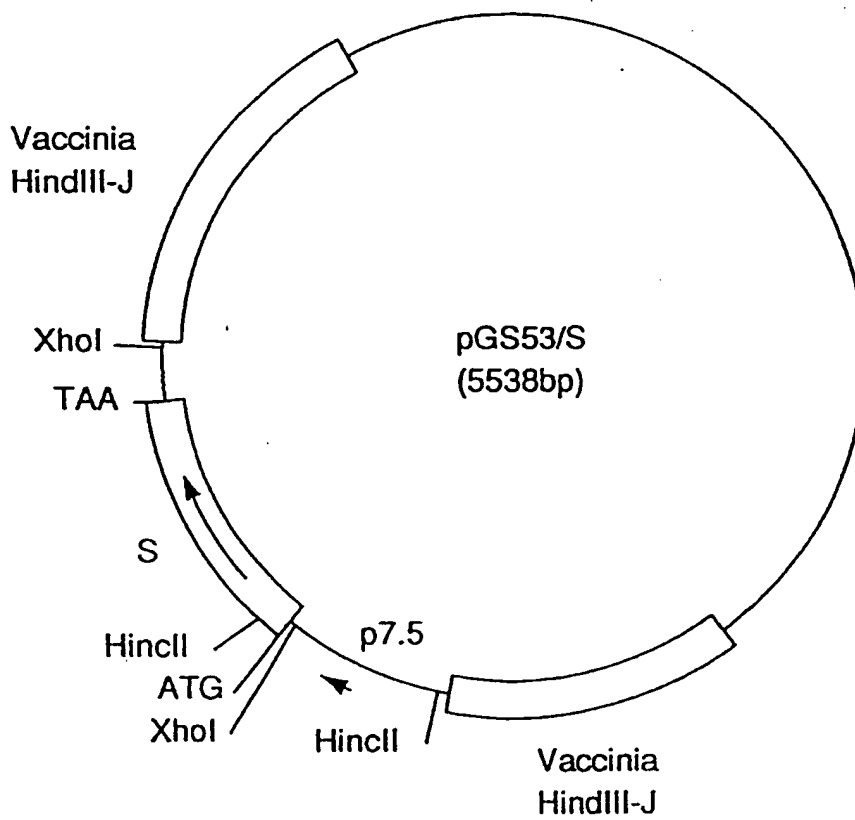
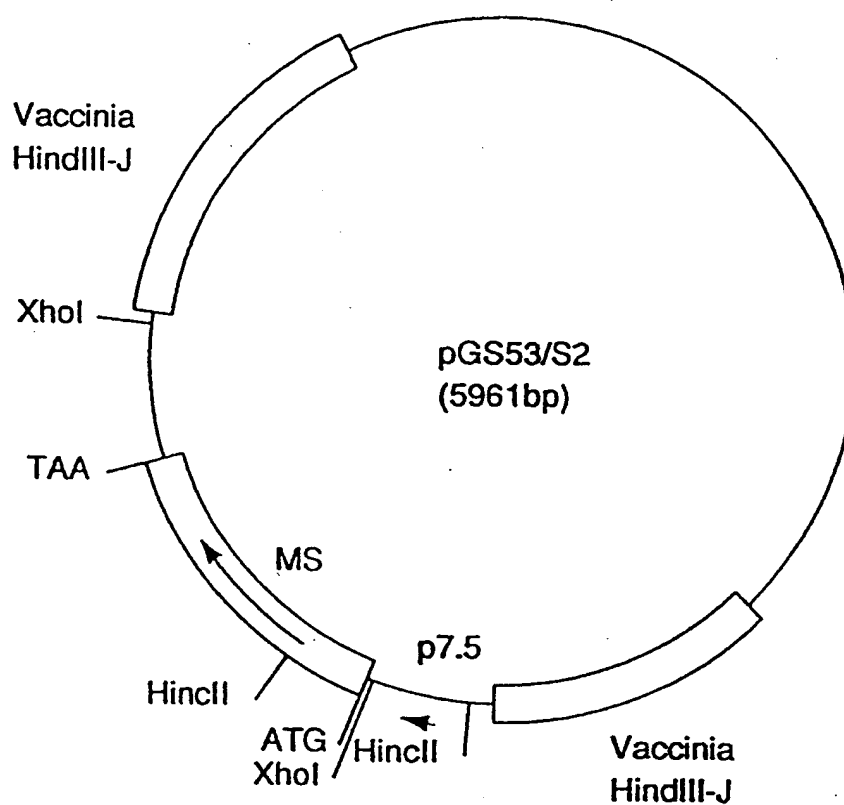


FIG. 35



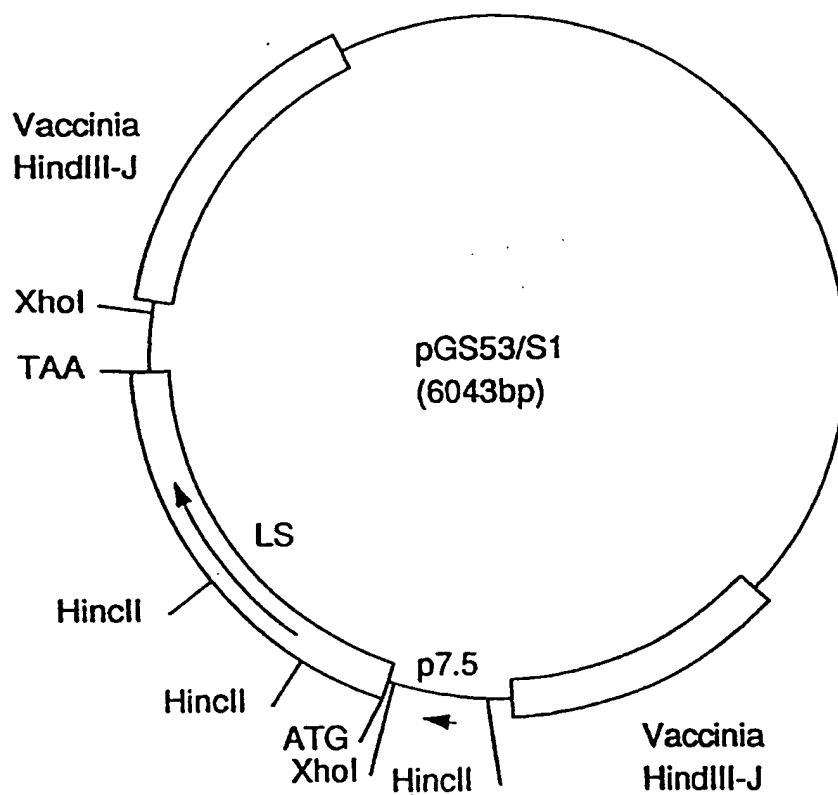
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FIG. 36



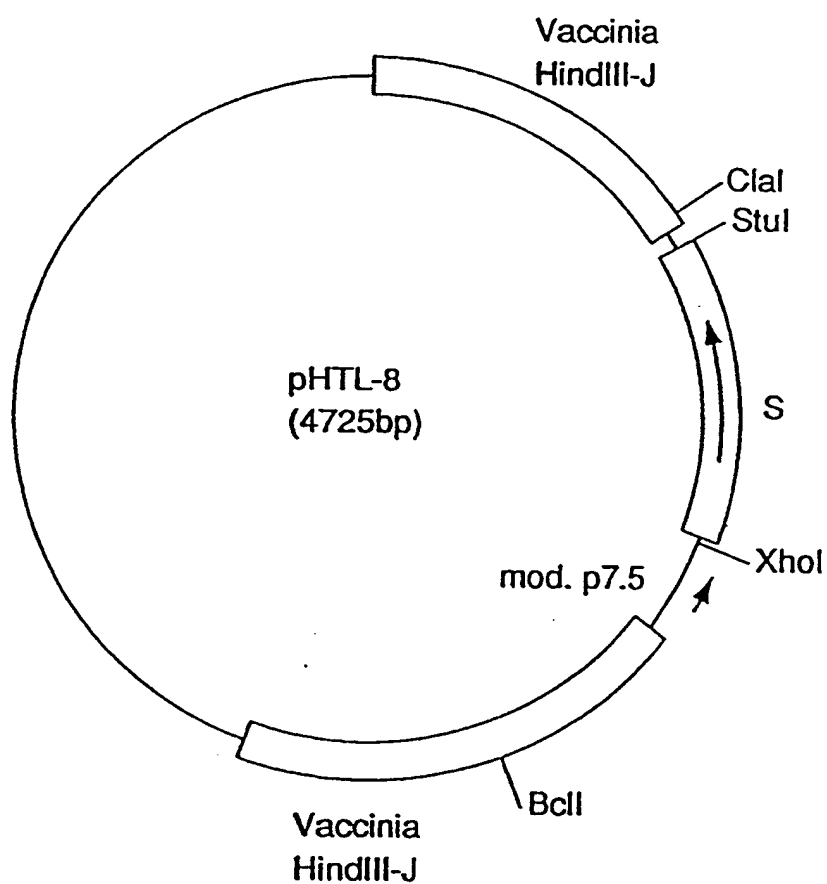
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FIG. 37



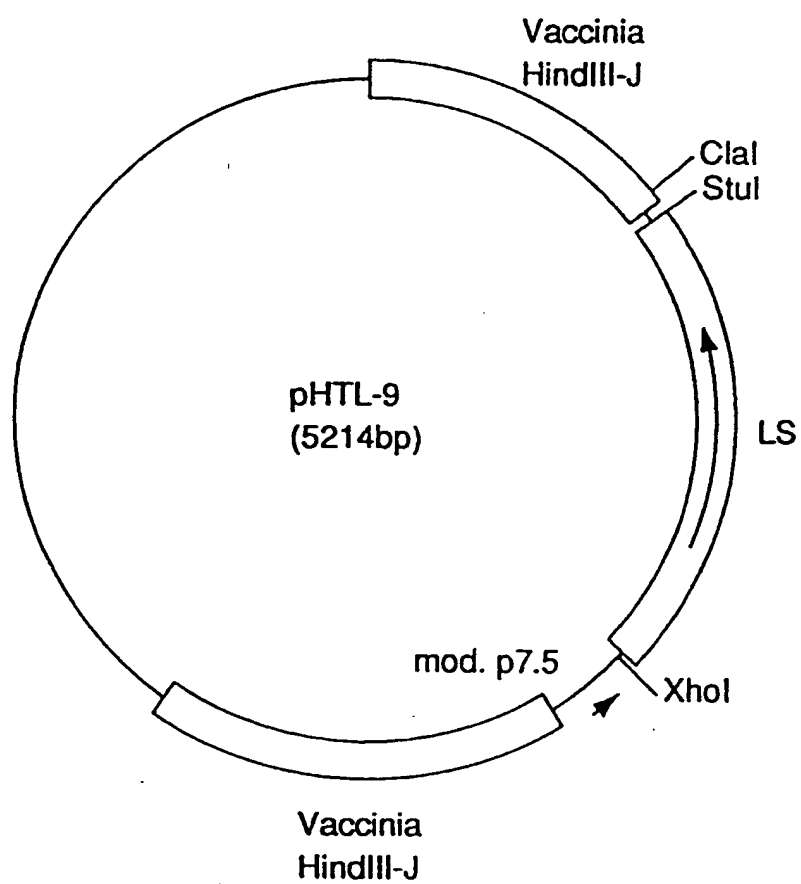
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FIG. 38



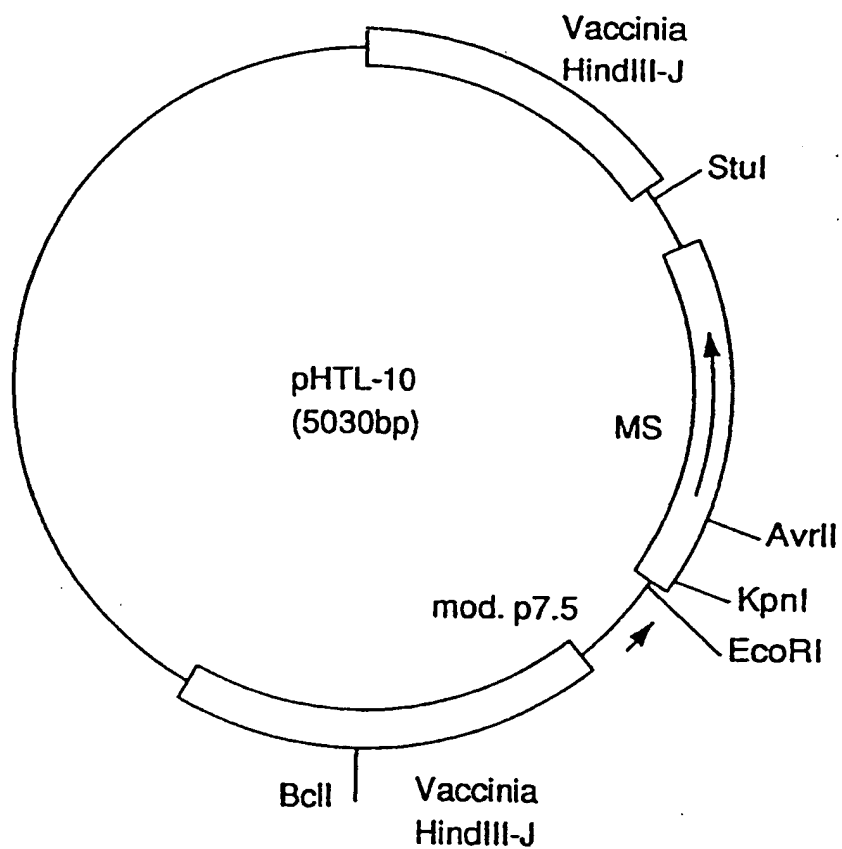
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FIG. 39



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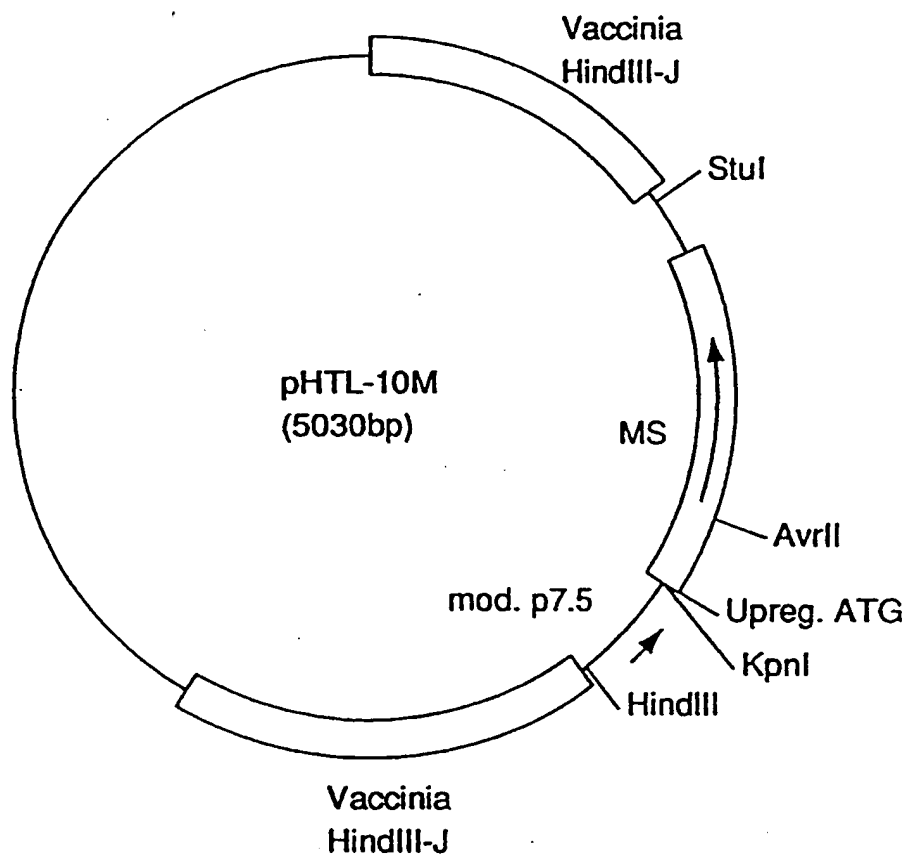
FIG. 40



SUBSTITUTE SHEET (RULE 26)

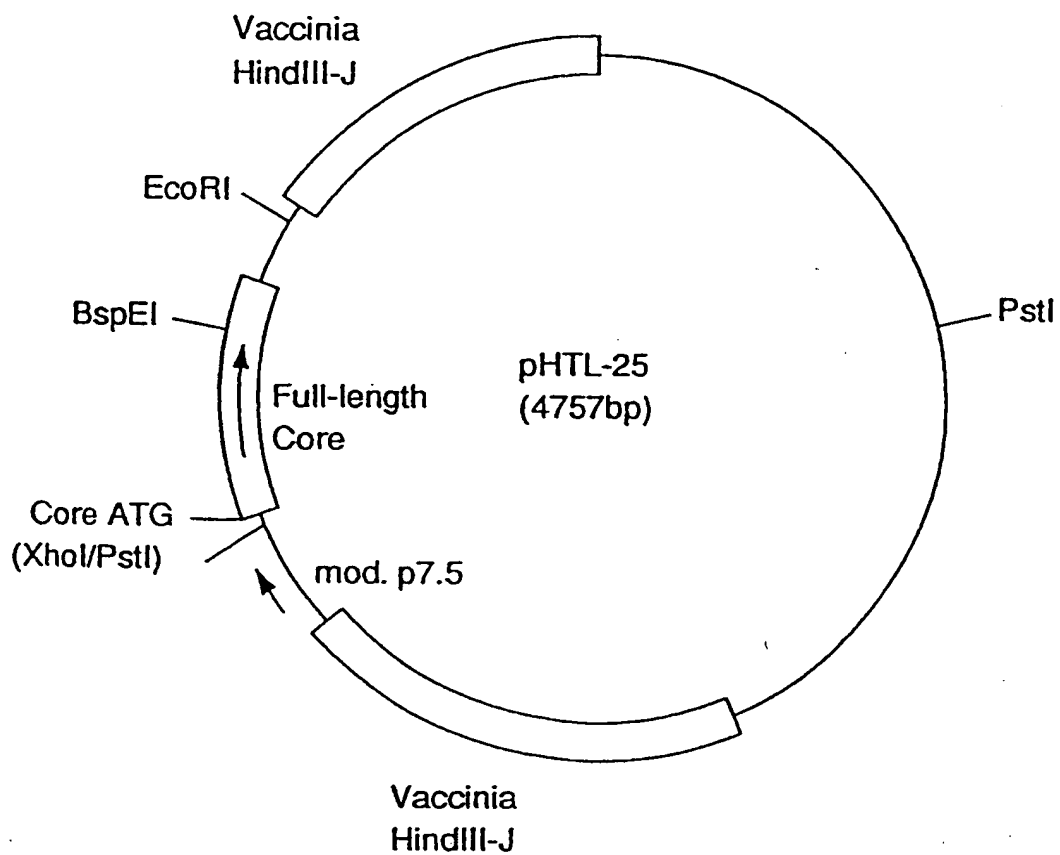
40/90

FIG. 41



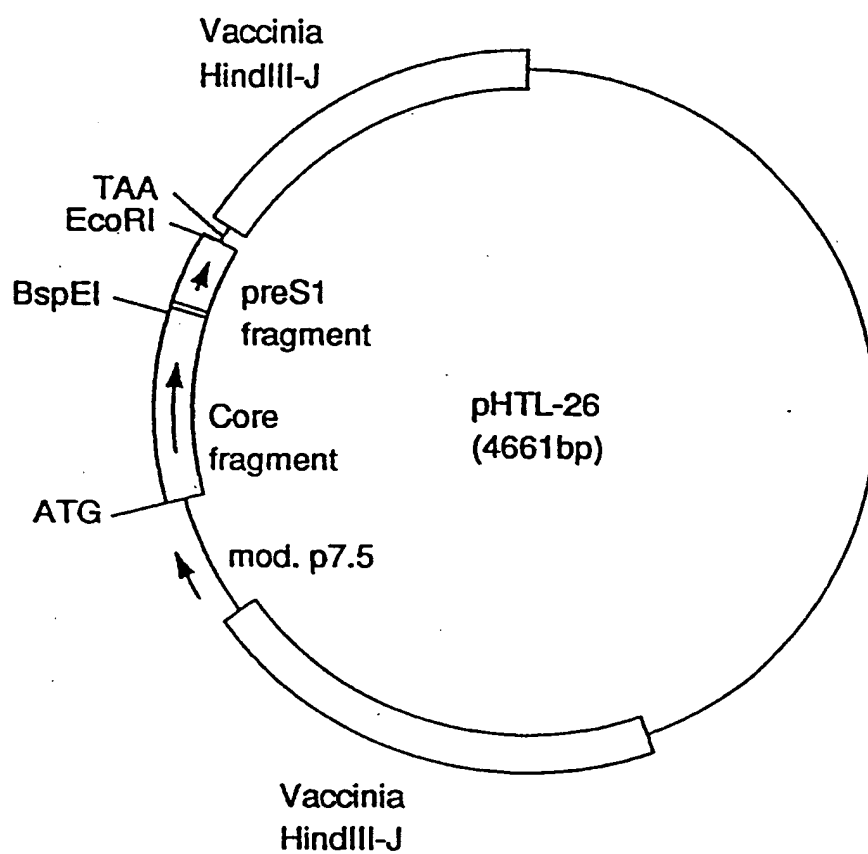
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FIG. 42



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FIG. 43



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1 / 1 31 / 11
ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC TCG TTT TTG CCT
met asp ile asp pro tyr lys glu phe gly ala thr val glu leu leu ser phe leu pro
61 / 21 91 / 31
TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC ACC GCC TCA GCT CTG TAT CCG GAA
ser asp phe phe pro ser val arg asp leu leu asp thr ala ser ala leu tyr arg glu
121 / 41 151 / 51
GCC TTA GAG TCT CCT GAG GAT TGC TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC
ala leu glu ser pro glu his cys ser pro his his thr ala leu arg gln ala ile leu
181 / 61 211 / 71
TGC TGG GGG GAA TTG ATG ACT CTA GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA
cys trp gly glu leu met thr leu ala thr trp val gly asn asn leu glu asp pro ala
241 / 81 271 / 91
TCA AGG GAT CTA GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA ATT AGG CAA CTA
ser arg asp leu val val asn tyr val asn thr asn met gly leu lys ile arg gln leu
301 / 101 331 / 111
TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA GAG ACT GTA CTT GAA TAT TTG GTA
leu trp phe his ile ser cys leu thr phe gly arg glu thr val leu glu tyr leu val
361 / 121 391 / 131
TCT TTC GGA GTG TGG ATT CCG ACT CCT CCA GCC TAT AGA CCA CCA AAT GCC CCT ATC TTA
ser phe gly val trp ile arg thr pro pro ala tyr arg pro pro asn ala pro ile leu
421 / 141 451 / 151
TCA ACA CTT CCG gaa tCa gcl tgc ATG GGG ACG AAT CTT TCT GTT CCC AAT CCT CTG GGA
ser thr leu pro glu ser ala cys met gly thr asn leu ser val pro asn pro leu gly
481 / 161 511 / 171
TTC LTT CCC GAT CAT CAG TTG GAC CCT GCA TTC GGA GCC AAC TCA Aac AAT CCA GAT TGC
phe phe pro asp his gln leu asp pro ala phe gly ala asn ser asn asn pro asp trp
541 / 181 571 / 191
GAC TTC AAC CCC ATC AAG GAC CAC TGG CCA GCA GCC AAC CAG GTA GGA GTG GGA GCA TTC
asp phe asn pro ile lys asp his trp pro ala ala asn gln val gly val gly ala phe
601 / 201
GGG CCA GAA TTC AGG CCT ACT AGT TAA
gly pro glu phe arg pro thr ser OCH

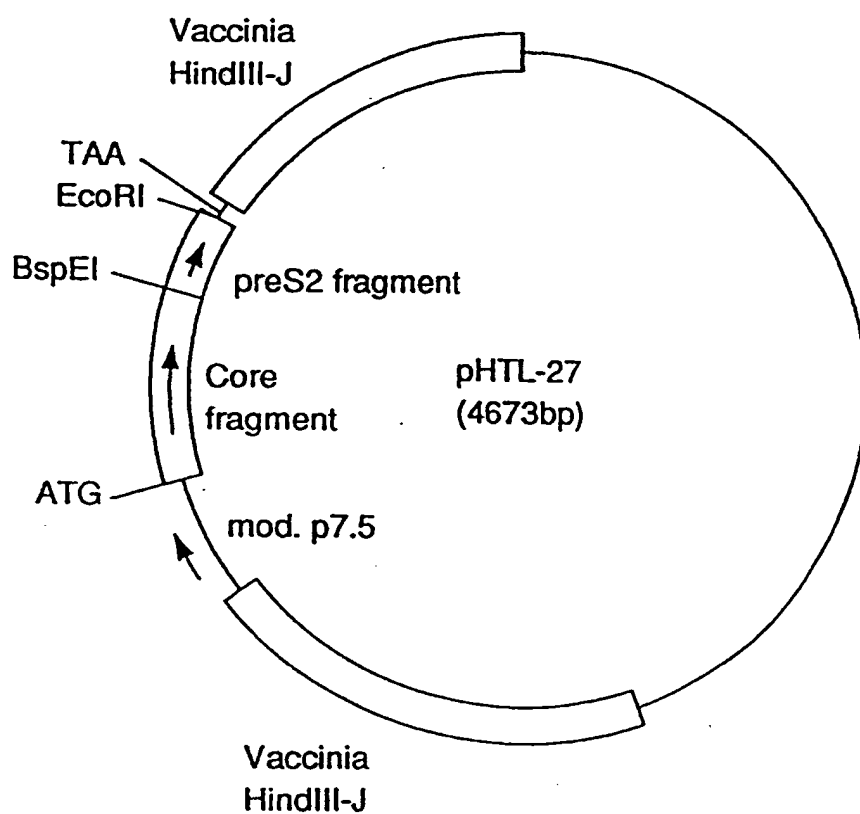
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FIG.44

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FIG. 45



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1 / 1 31 / 11
ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC TCG TTT TTG CCT
met asp ile asp pro tyr lys glu phe gly ala thr val glu leu leu ser phe leu pro
61 / 21 91 / 31
TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC ACC GCC TCA GCT CTG TAT CGG GAA
ser asp phe phe pro ser val arg asp leu leu asp thr ala ser ala leu tyr arg glu
121 / 41 151 / 51
GCC TTA GAG TCT CCT GAG CAT TGC TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC
ala leu glu ser pro glu his cys ser pro his his thr ala leu arg gln ala ile leu
181 / 61 211 / 71
TGC TGG GGG GAA TTG ATG ACT CTA GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA
cys trp gly glu leu met thr leu ala thr trp val gly asn asn leu glu asp pro ala
241 / 81 271 / 91
TCA AGG GAT CTA GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA ATT AGG CAA CTA
ser arg asp leu val val asn tyr val asn thr asn met gly leu lys ile arg gln leu
301 / 101 331 / 111
TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA GAG ACT GTA CTT GAA TAT TTG GTA
leu trp phe his ile ser cys leu thr phe gly arg glu thr val leu glu tyr leu val
361 / 121 391 / 131
TCT TTC GGA GTG TGG ATT CGC ACT CCT CCA GCC TAT AGA CCA CCA AAT GCC CCT ATC TTA
ser phe gly val trp ile arg thr pro pro ala tyr arg pro pro asn ala pro ile leu
421 / 141 451 / 151
TCA ACA CTT CCG GAC ATG CAG TGG AAC TCC ACT GCC TTC CAC CAA GCT CTG CAG GAT CCC
ser thr leu pro asp met gln trp asn ser thr ala phe his gln ala leu gln asp pro
481 / 161 511 / 171
AGA GTC AGG GGT CTG TAT TTT CCT GCT GGT GGC TCC AGT TCA GGA ACA GTA AAC CCT GCT
arg val arg gly leu tyr phe pro ala gly gly ser ser ser gly thr val asn pro ala
541 / 181 571 / 191
CCG AAT ATT GCC TCT CAC ATC TCG TCA ATC TCC GCG AGG ACT GCG GAC CCT GTG ACG ACG
pro asn ile ala ser his ile ser ser ile ser ala arg thr gly asp pro val thr asn
601 / 201 631 / 211
ATG GAG AAC ATC ACA TCA GAA TTC AGG CCT ACT AGT TAA
met glu asn ile thr ser glu phe arg pro thr ser OCH

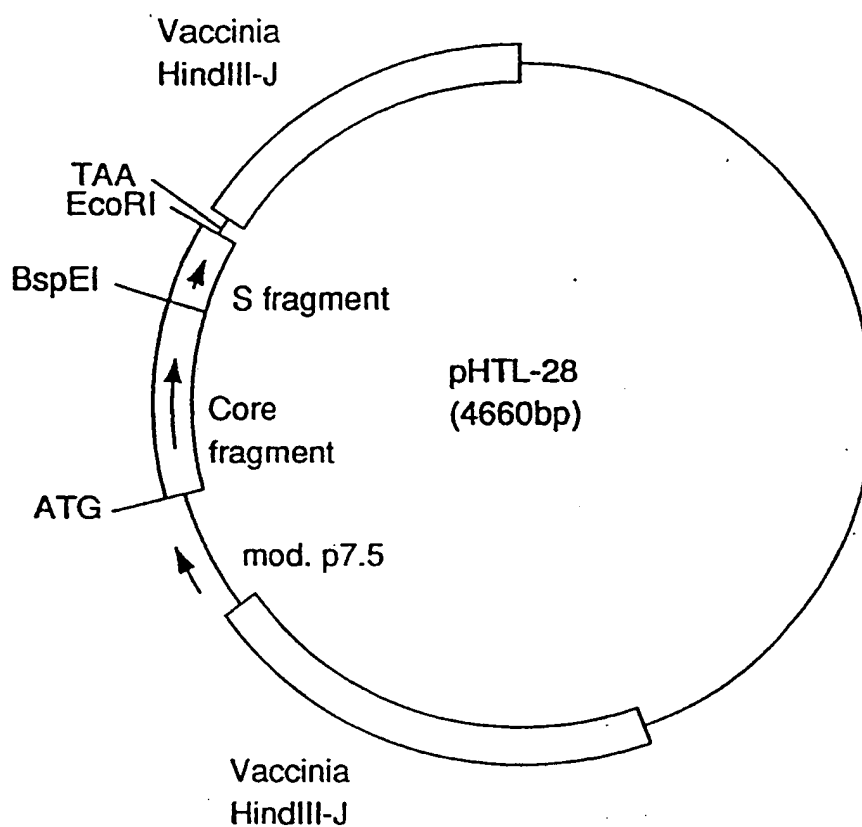
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FIG.46

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FIG. 47



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1   /   1                               31  /   11
ATG GAC ATT GAC CCT TAT AAA GAA TTT GGA GCT ACT GTG GAG TTA CTC TCG TTT TTG CCT
mel asp ile asp pro tyr lys glu phe gly ala thr val glu leu leu ser phe leu pro
61  /   21                               91  /   31
TCT GAC TTC TTT CCT TCC GTC AGA GAT CTC CTA GAC ACC GCC TCA GCT CTG TAT CCG GAA
ser asp phe phe pro ser val arg asp leu leu asp thr ala ser ala leu tyr arg glu
121 /   41                               151 /   51
GCC TTA GAG TCT CCT GAG CAT TGC TCA CCT CAC CAC ACC GCA CTC AGG CAA GCC ATT CTC
ala leu glu ser pro glu his cys ser pro his his thr ala leu arg gln ala ile leu
181 /   61                               211 /   71
TGC TGG GGG GAA TTG ATG ACT CTA GCT ACC TGG GTG GGT AAT AAT TTG GAG GAT CCA GCA
cys trp gly glu leu met thr leu ala thr trp val gly asn asn leu glu asp pro ala
241 /   81                               271 /   91
TCA AGG GAT CTA GTA GTC AAT TAT GTT AAT ACT AAC ATG GGT TTA AAA ATT AGG CAA CTA
ser arg asp leu val val asn tyr val asn thr asn met gly leu lys ile arg gln leu
301 /  101                               331 /  111
TTG TGG TTT CAT ATA TCT TGC CTT ACT TTT GGA AGA GAG ACT GTA CTT GAA TAT TTG GTA
leu trp phe his ile ser cys leu thr phe gly arg glu thr val leu glu tyr leu val
361 /  121                               391 /  131
TCT TTC GGA GTG TGG ATT CGC ACT CCT CCA GCC TAT AGA CCA CCA AAT GCC CCT ATC TTA
ser phe gly val trp ile arg thr pro pro ala tyr arg pro pro asn ala pro ile leu
421 /  141                               451 /  151
TCA ACA CTT CCG GAT TGT CCT CTA ATT CCA GGA TCA ACA ACA ACC AGT ACG GGA CCA TGC
ser thr leu pro asp cys pro leu ile pro gly ser thr thr thr ser thr gly pro cys
481 /  161                               511 /  171
AAA ACC TGC ACG ACT CCT GCT CAA GGC AAC TCT ATG TTT CCC TCA TGT TGC TGT ACA AAA
lys thr cys thr thr pro ala gln gly asn ser met phe pro ser cys cys cys thr lys
541 /  181                               571 /  191
CCT ACG GAT GGA AAT TGC ACC TGT ATT CCC ATC CCA TCG TCT TGG GCT TTC GCA AAA TAC
pro thr asp gly asn cys thr cys ile pro ile pro ser ser trp ala phe ala lys tyr
601 /  201
CTA TGG AAT TCA GGC CTA CTA GTT AAG TAA
leu trp asn ser gly leu leu val lys

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FIG.48

SUBSTITUTE SHEET (RULE 26)

FIG. 49

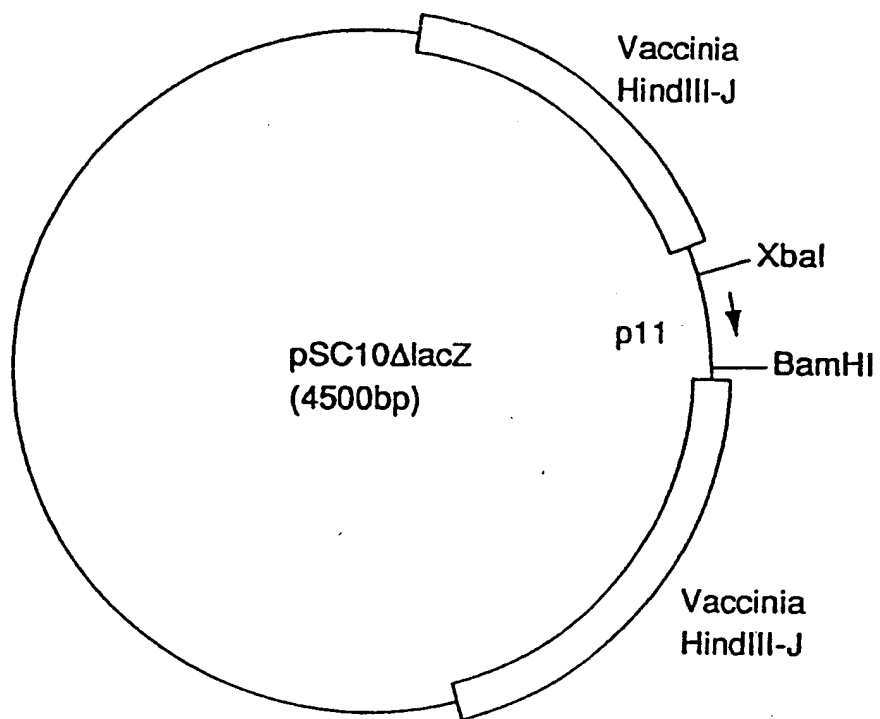
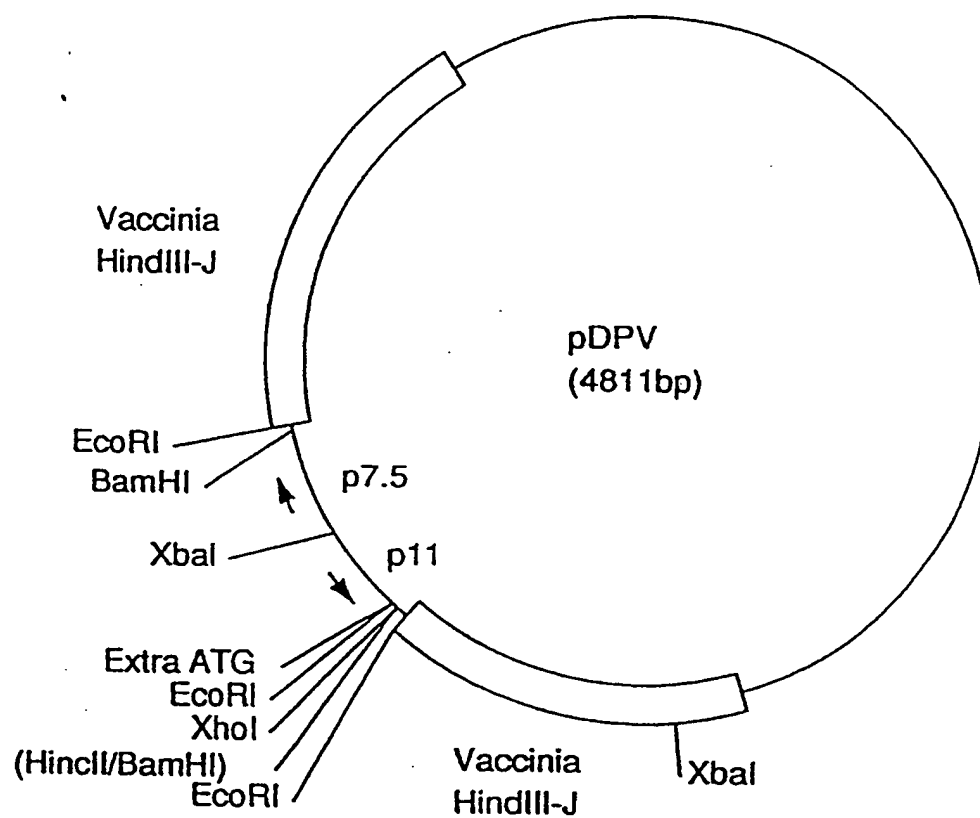
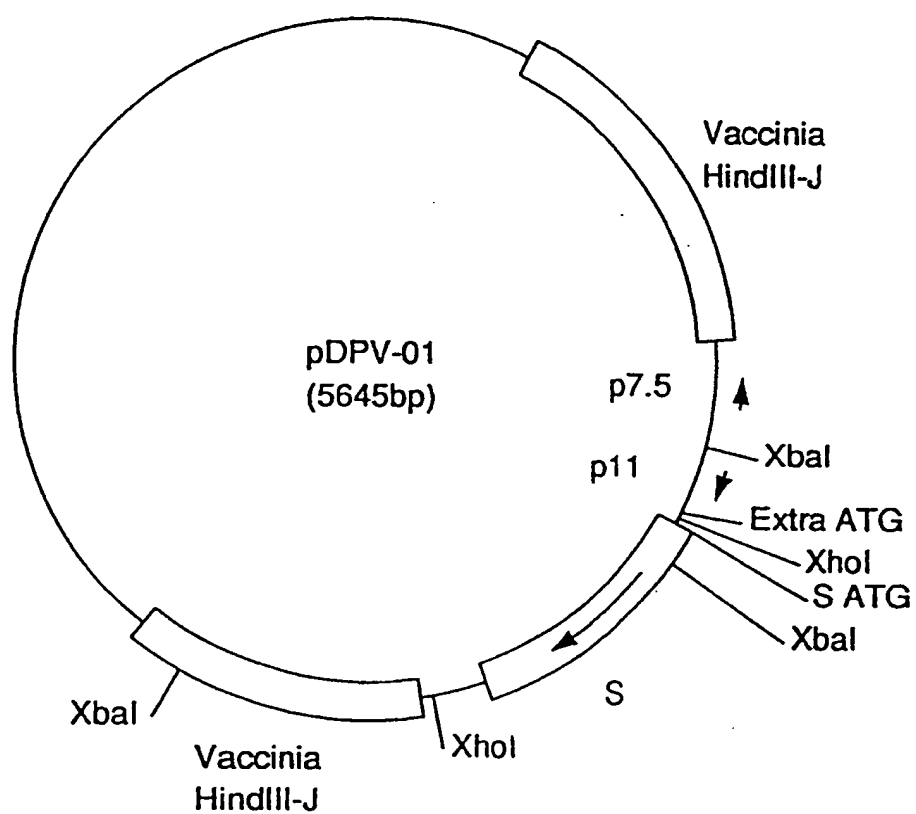


FIG. 50



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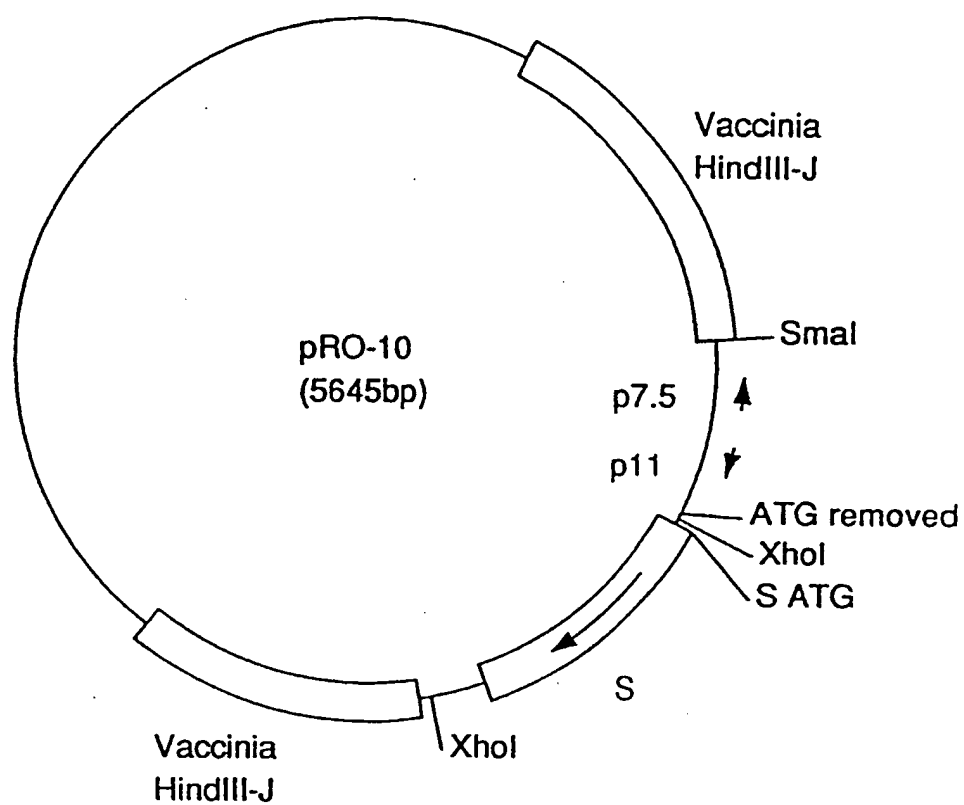
FIG. 51



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FIG. 52



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FIG. 53

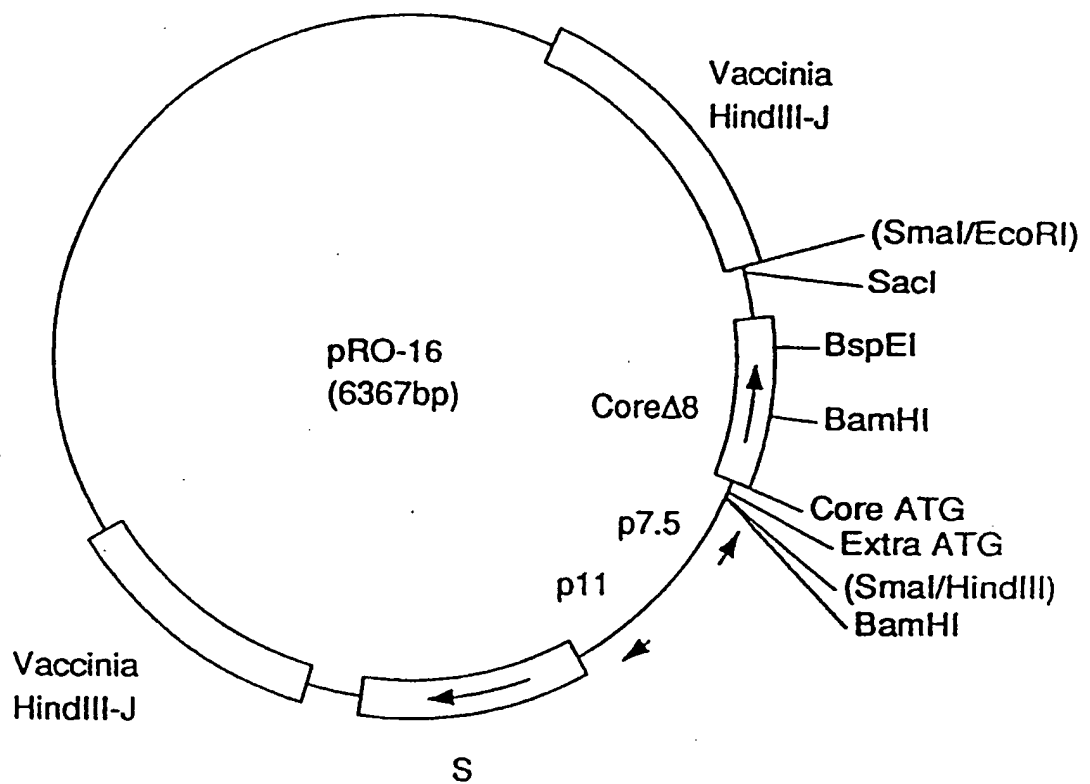
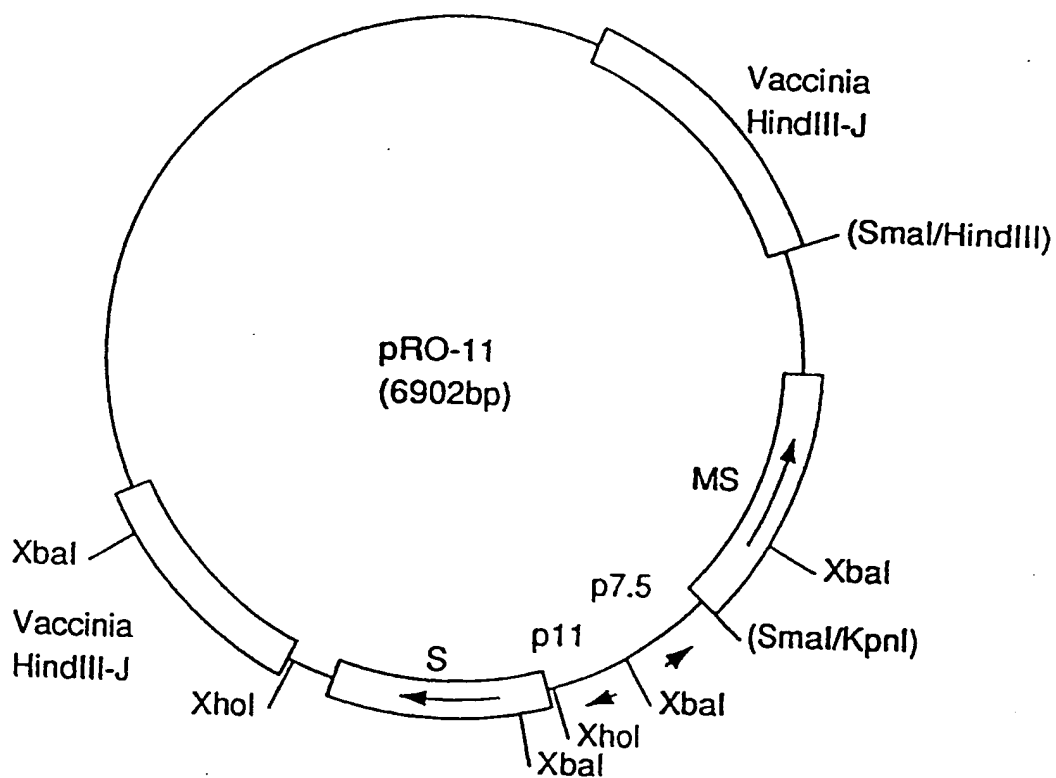
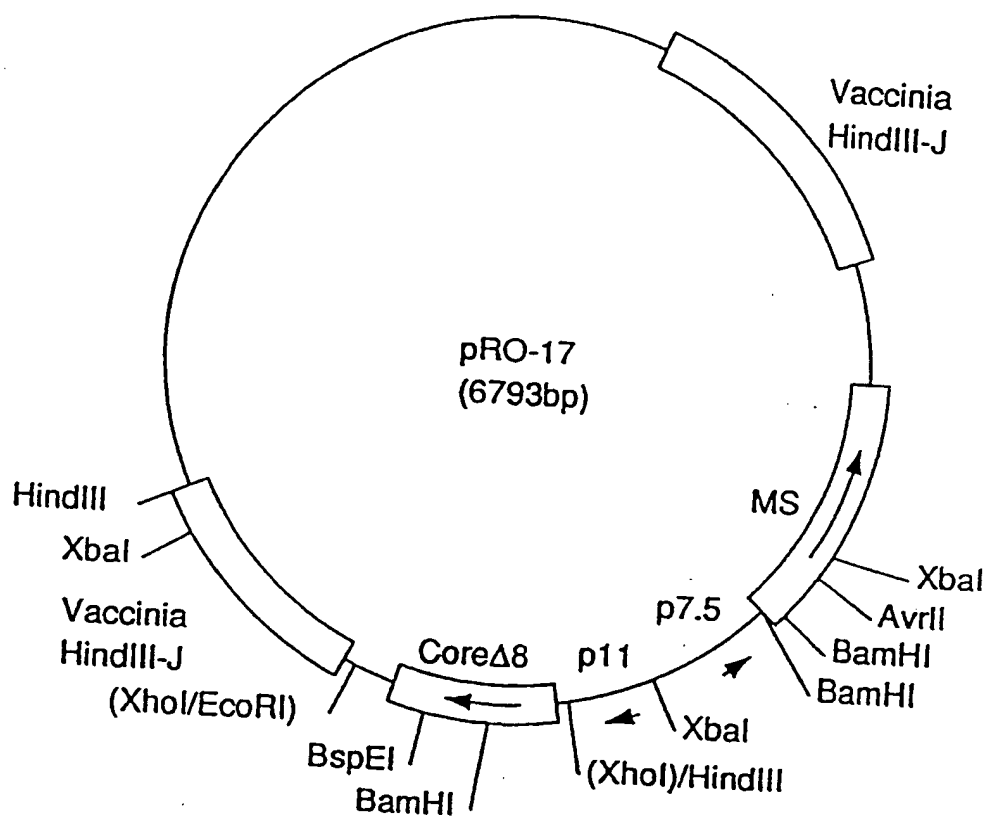


FIG. 54



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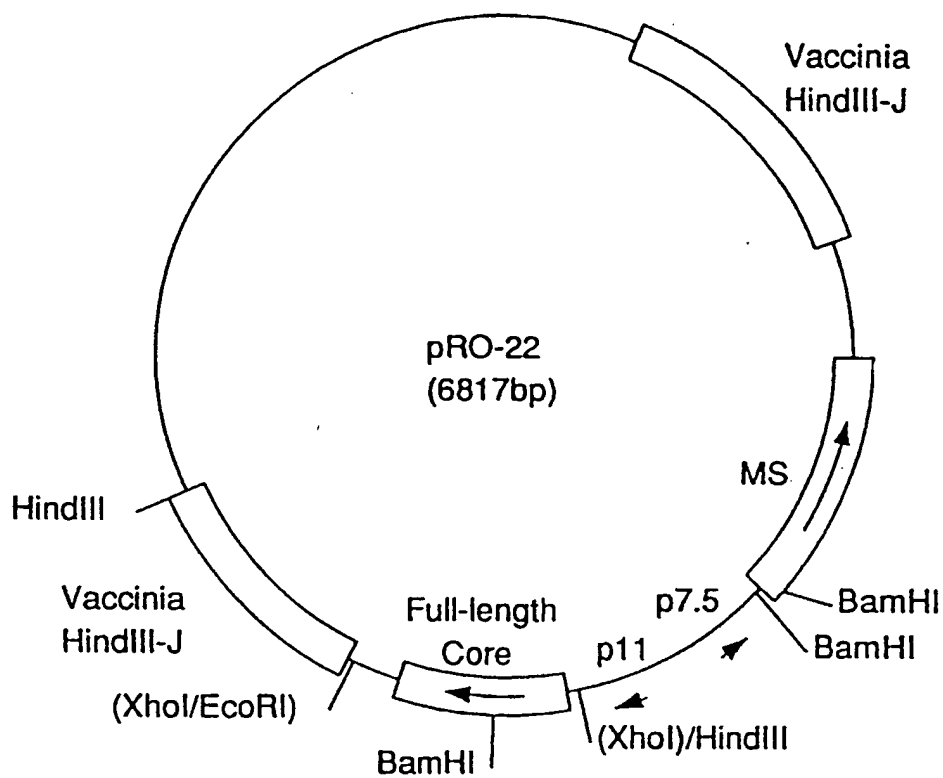
FIG. 55



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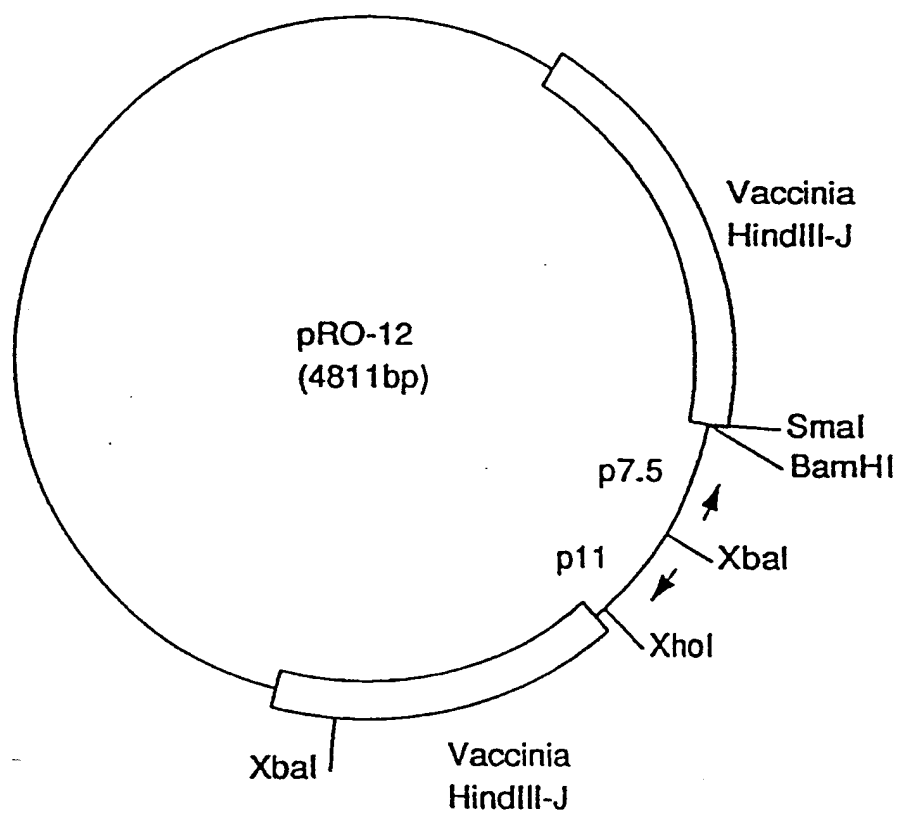
FIG. 56



SUBSTITUTE SHEET (RULE 26)

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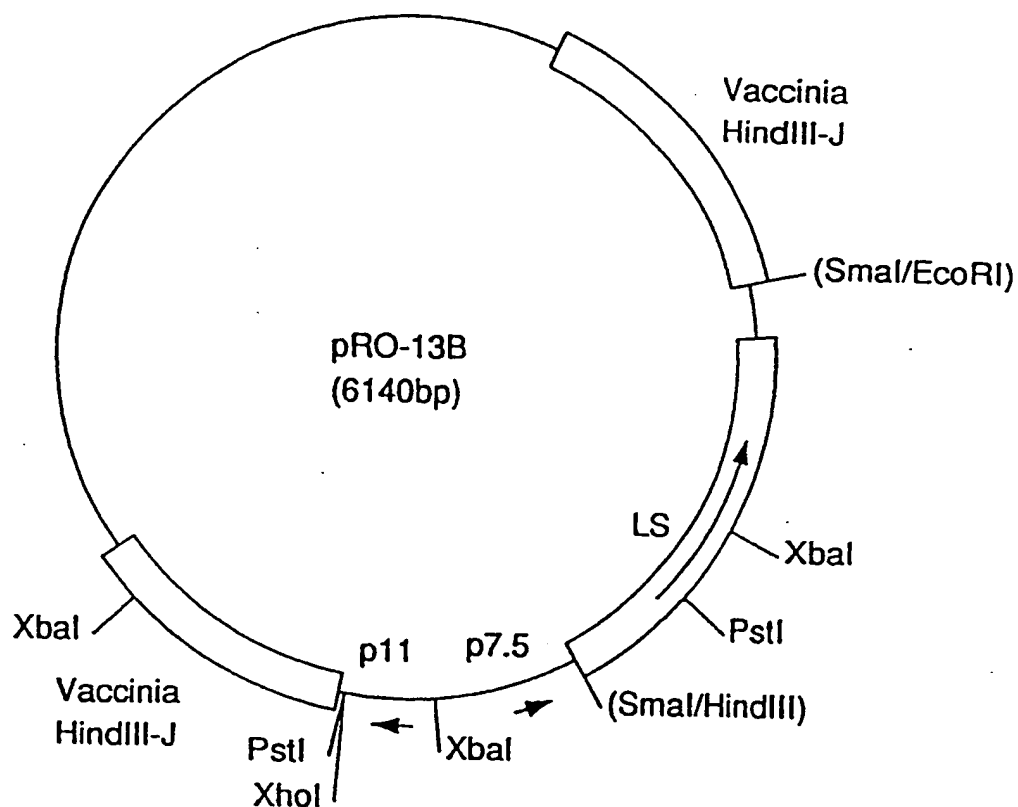
FIG. 57



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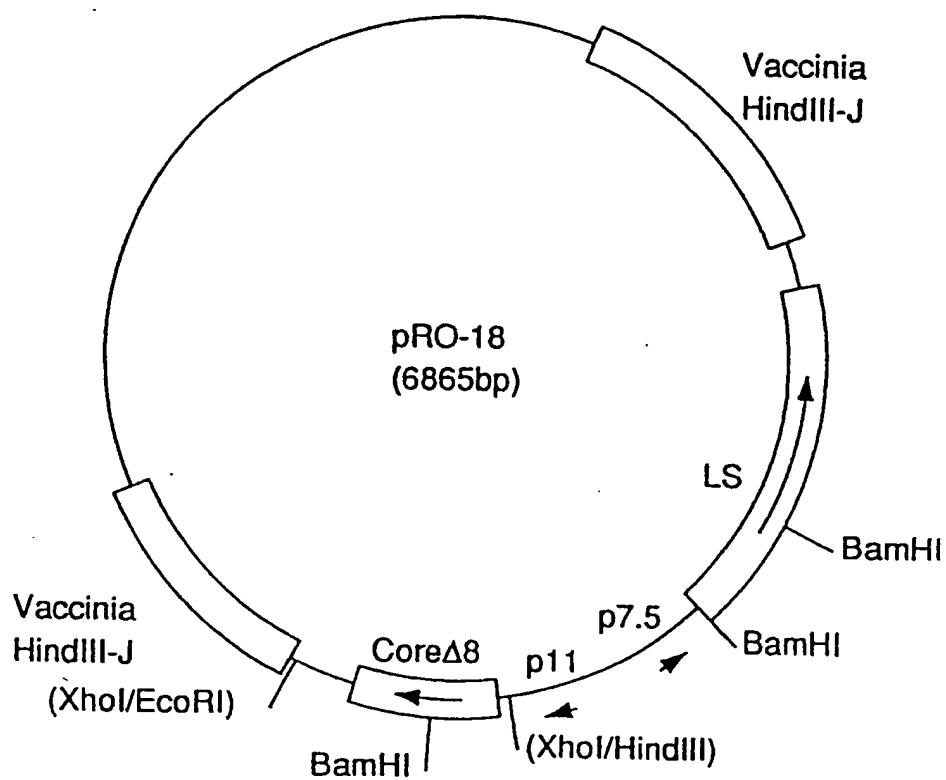
FIG. 58



SUBSTITUTE SHEET (RULE 26)

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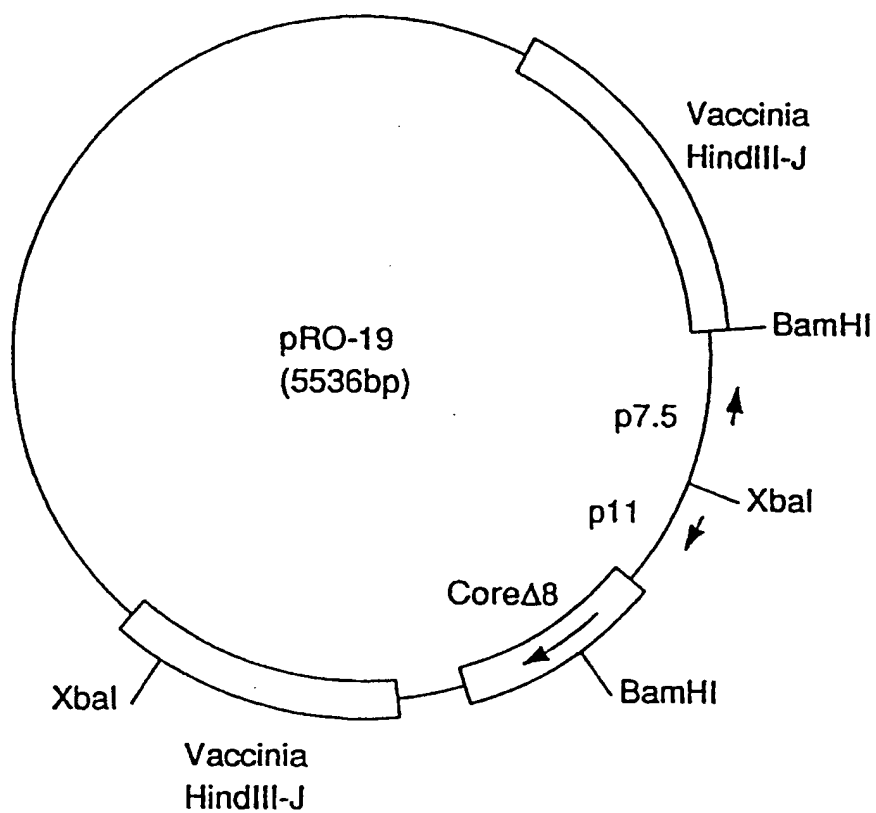
FIG. 59



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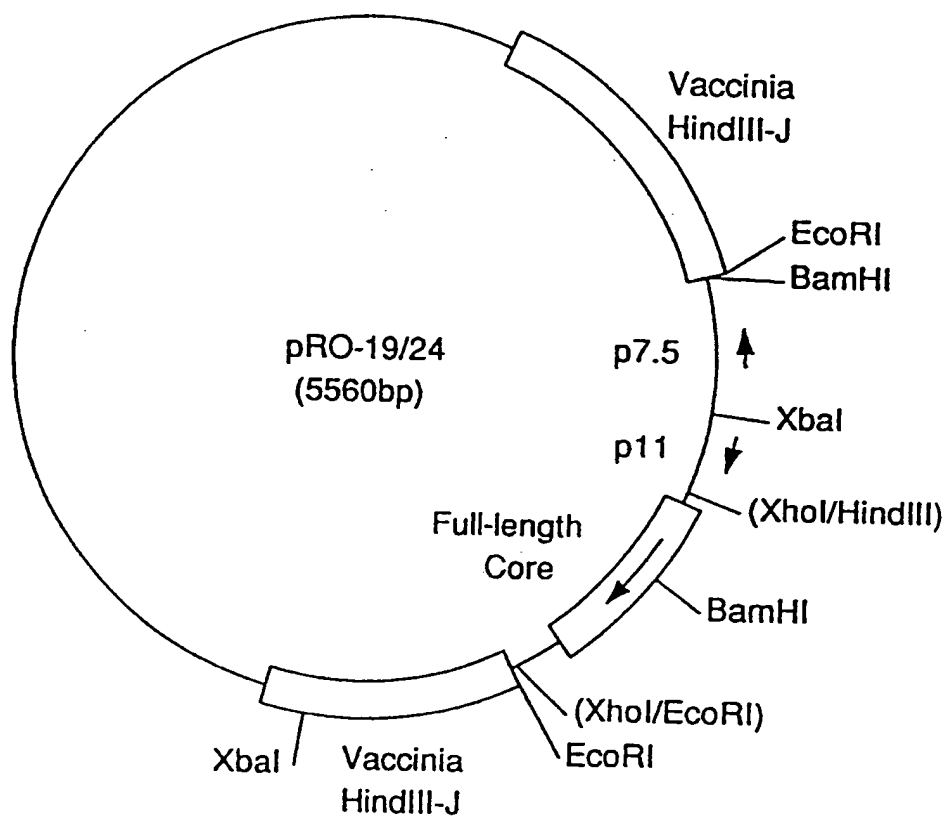
FIG. 60



SUBSTITUTE SHEET (RULE 26)

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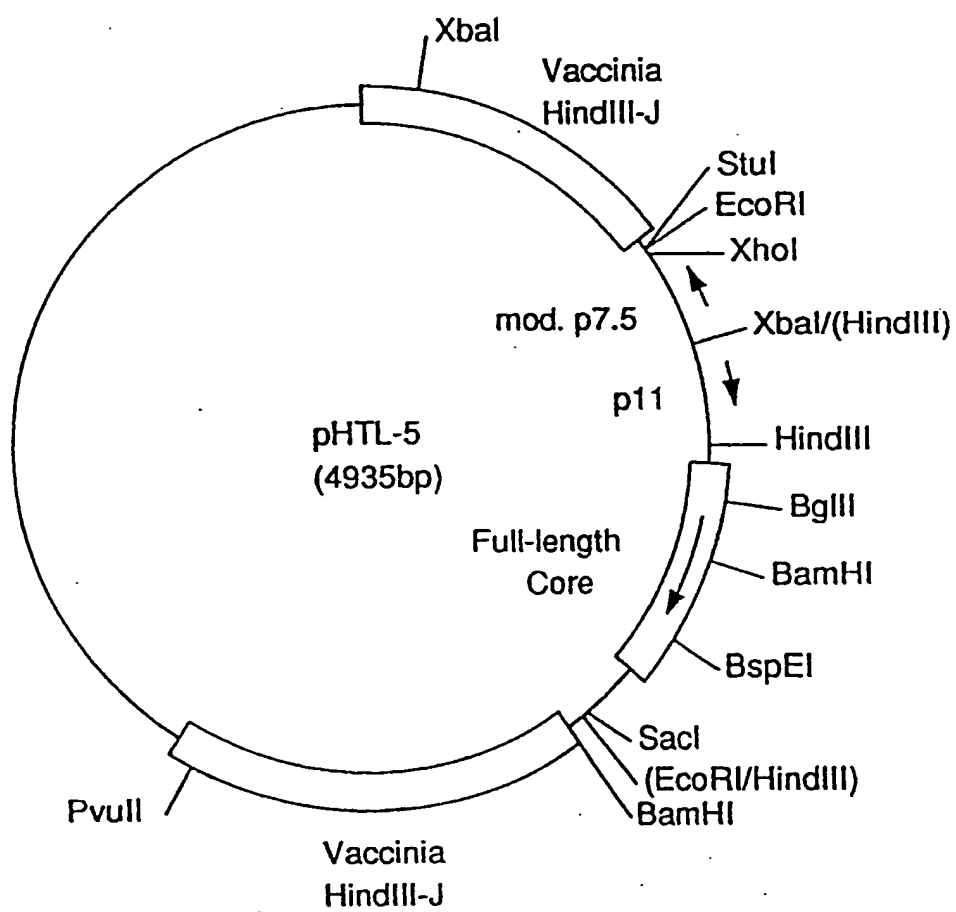
FIG. 61



SUBSTITUTE SHEET (RULE 26)

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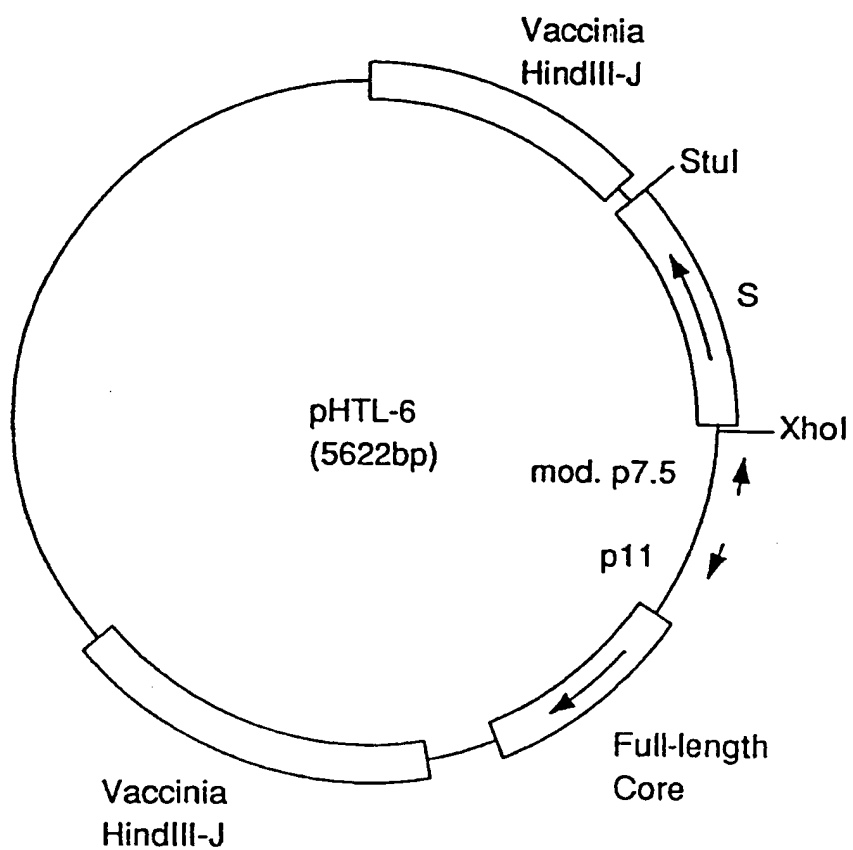
FIG. 62



SUBSTITUTE SHEET (RULE 26)

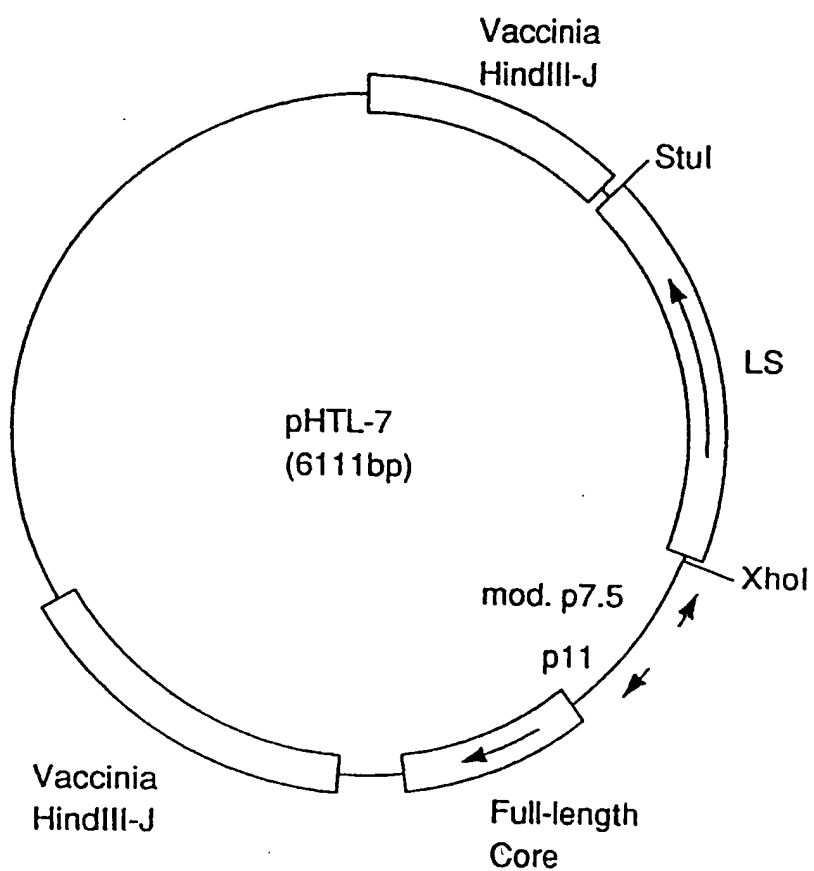
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FIG. 63



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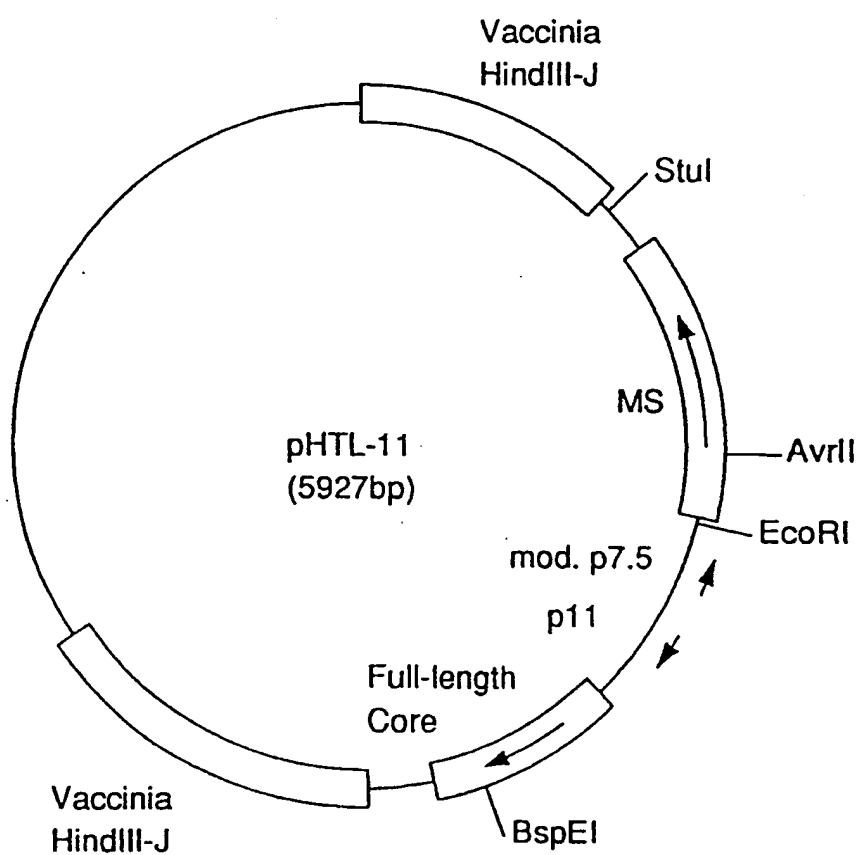
FIG. 64



SUBSTITUTE SHEET (RULE 26)

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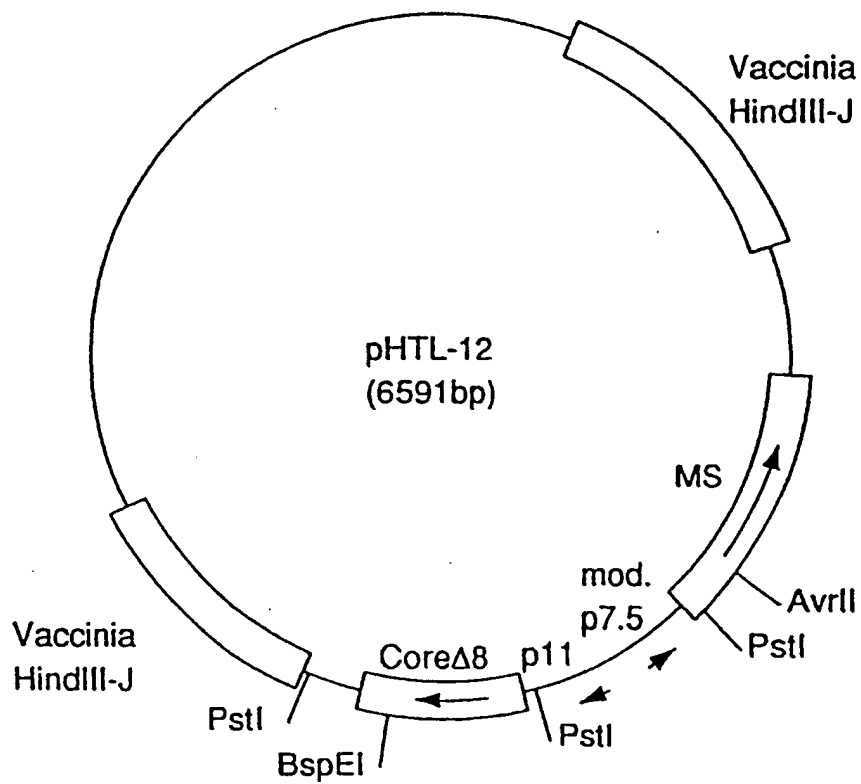
FIG. 65



SUBSTITUTE SHEET (RULE 26)

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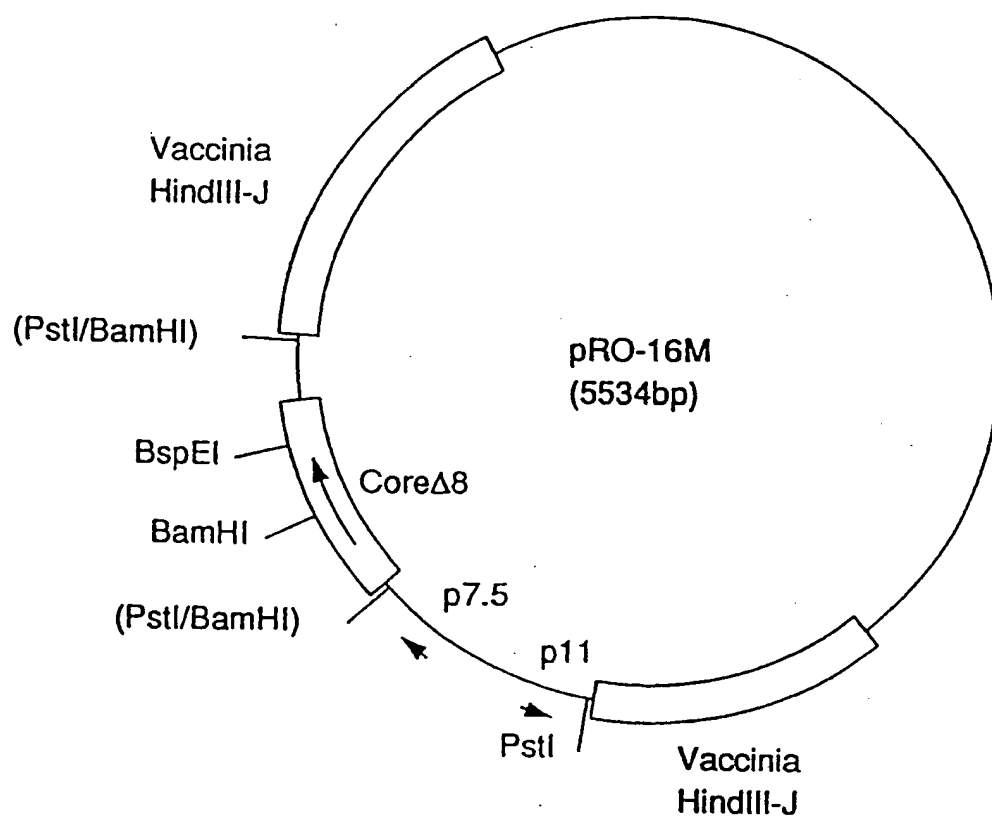
FIG. 66



SUBSTITUTE SHEET (RULE 26)

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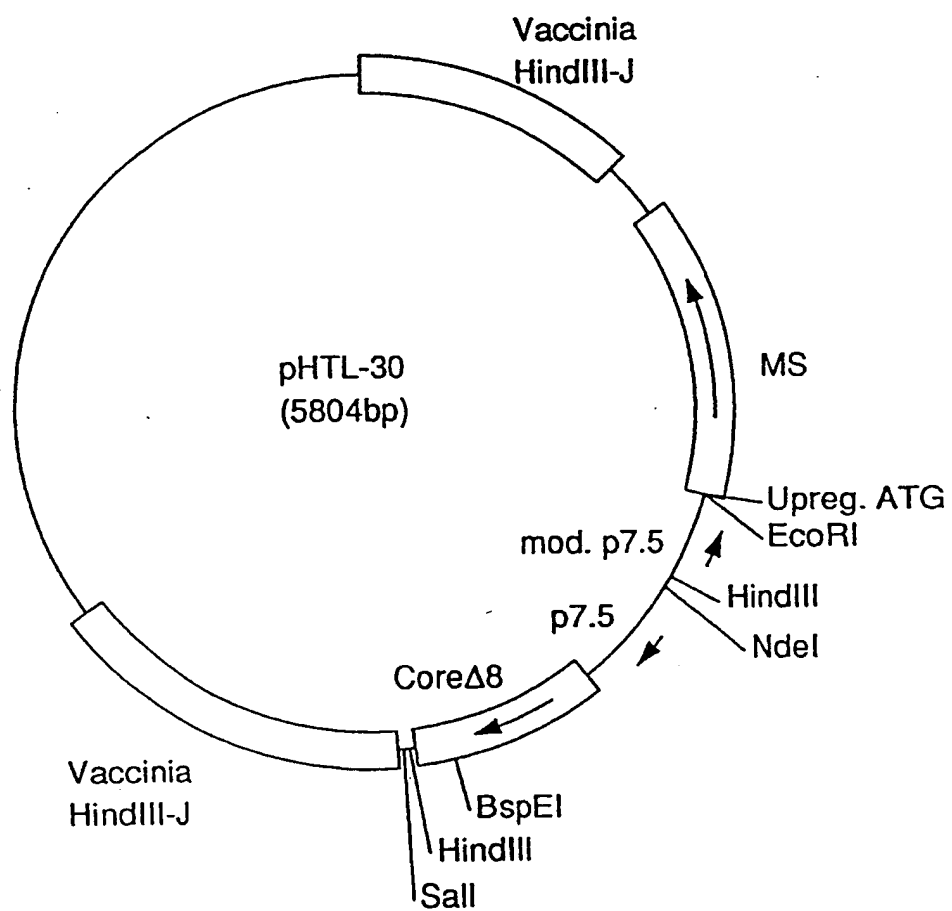
FIG. 67



SUBSTITUTE SHEET (RULE 26)

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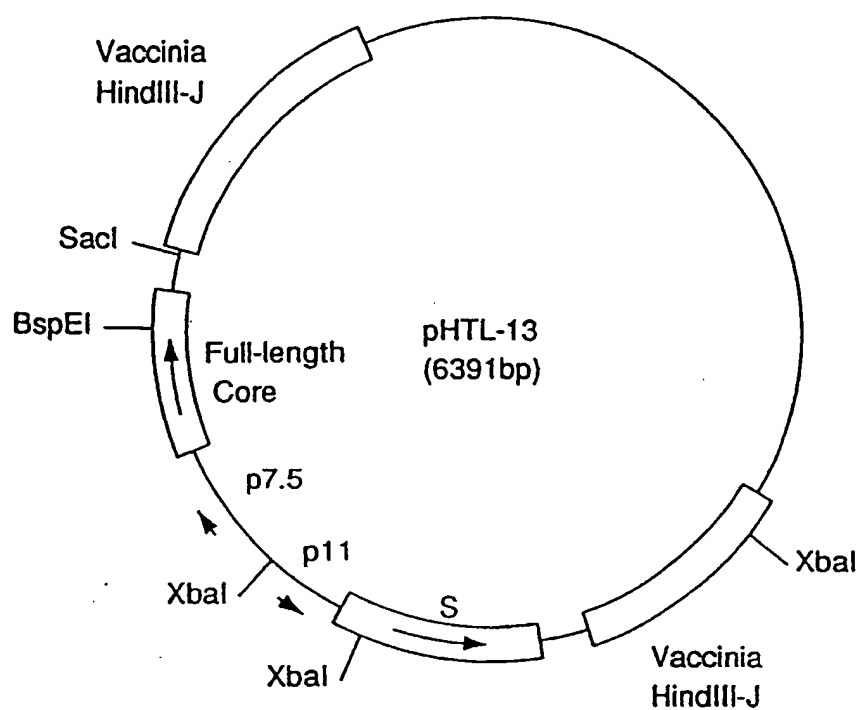
FIG. 68



SUBSTITUTE SHEET (RULE 26)

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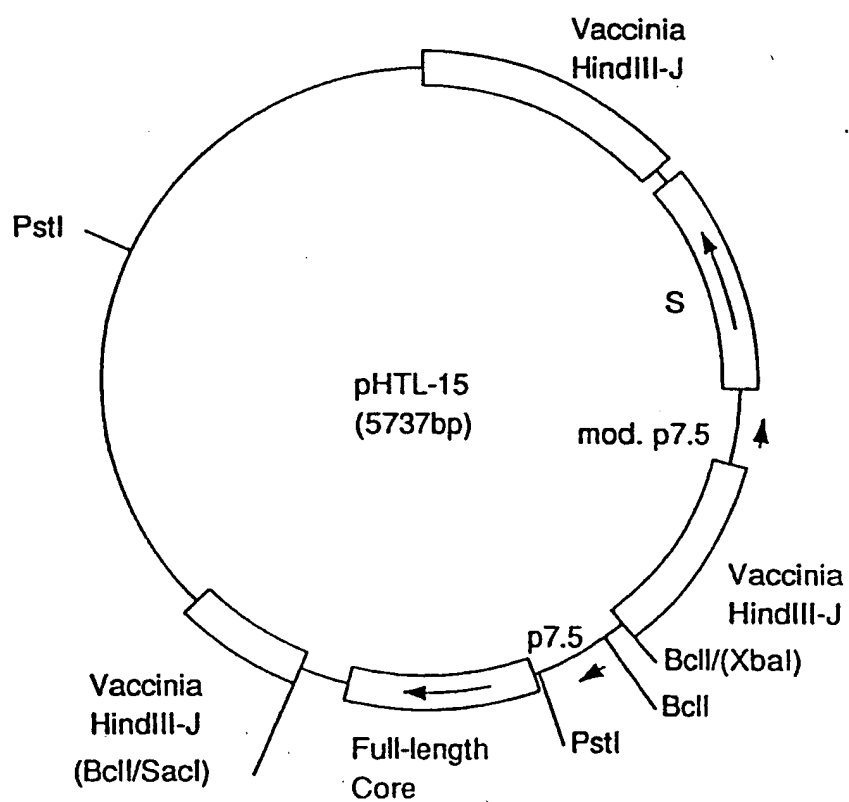
FIG. 69



SUBSTITUTE SHEET (RULE 26)

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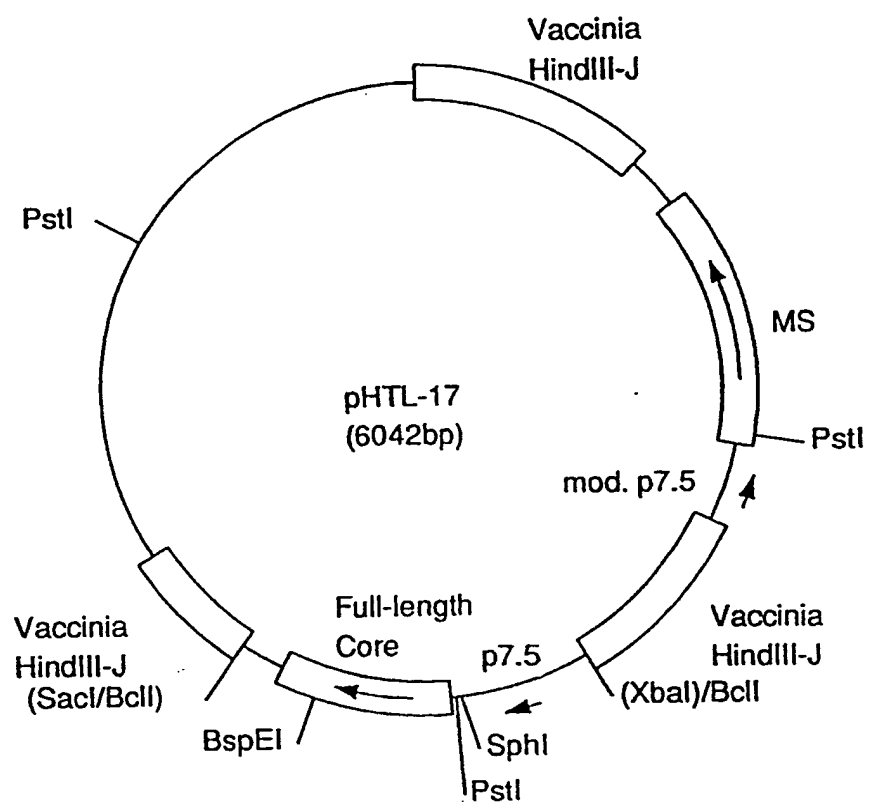
FIG. 70



SUBSTITUTE SHEET (RULE 26)

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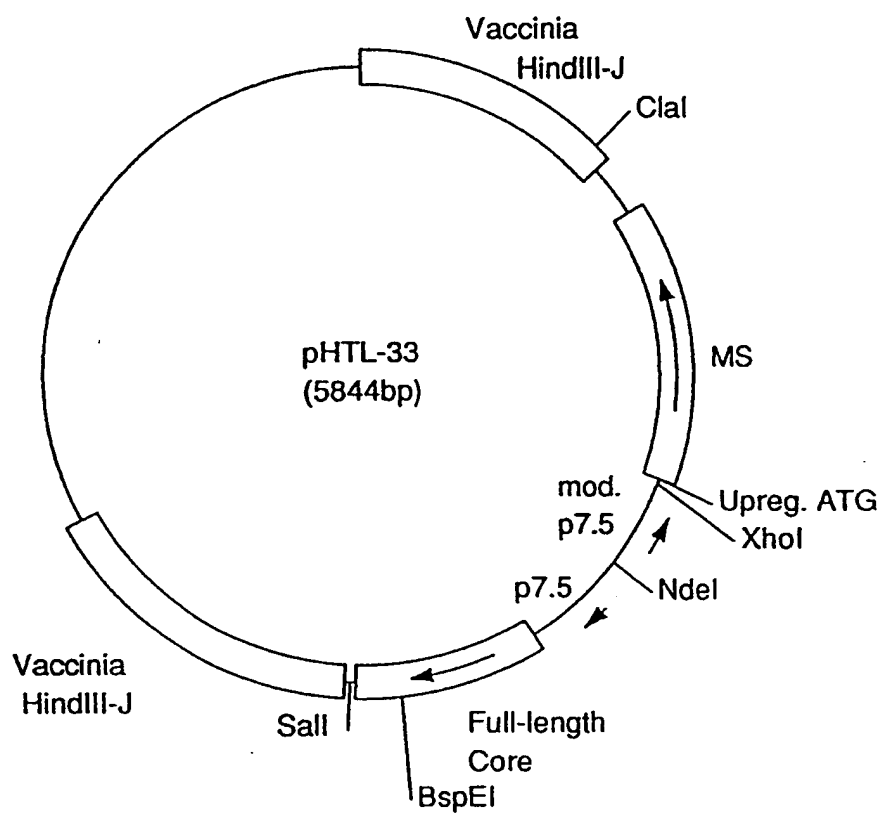
FIG. 71



SUBSTITUTE SHEET (RULE 26)

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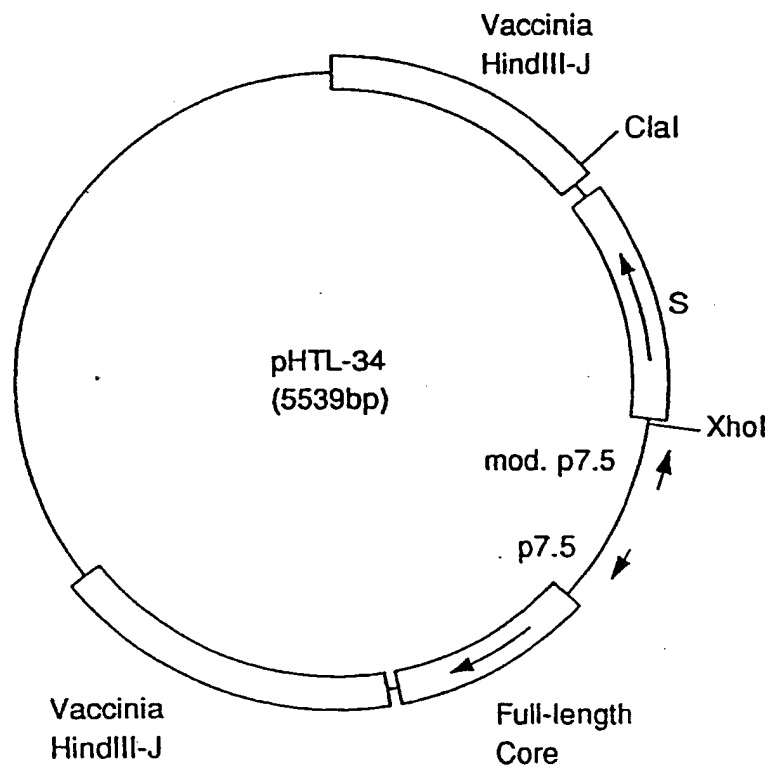
FIG. 72



SUBSTITUTE SHEET (RULE 26)

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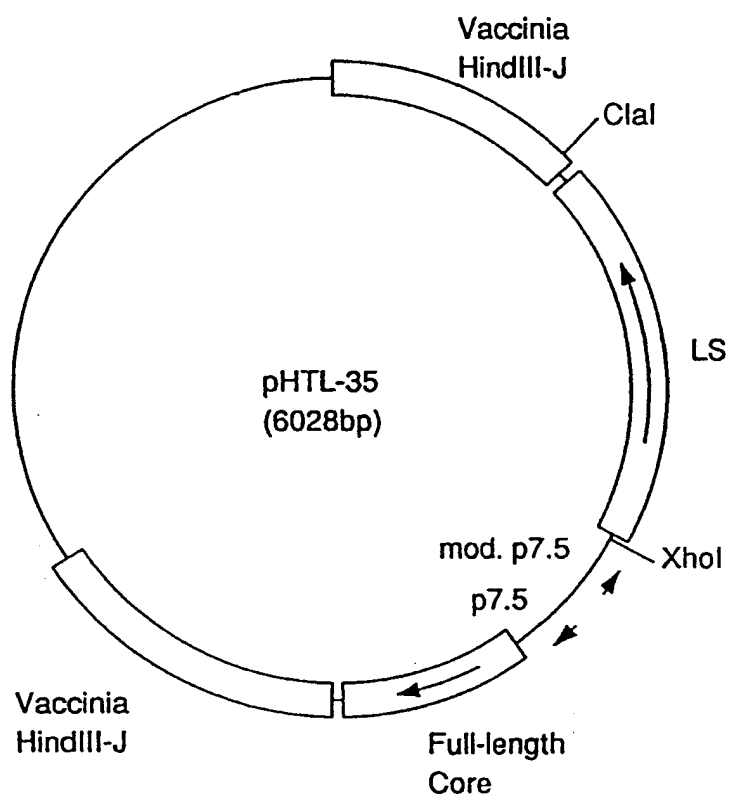
FIG. 73



SUBSTITUTE SHEET (RULE 26)

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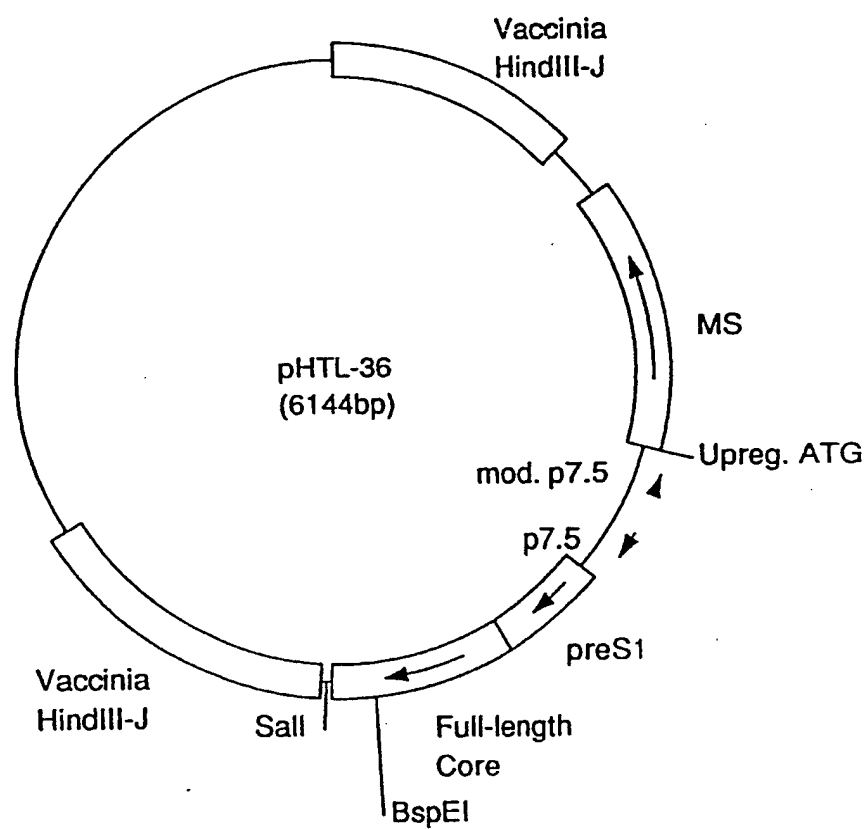
FIG. 74



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FIG. 75



SUBSTITUTE SHEET (RULE 26)